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"A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified human salivary gland adenocarcinoma.";
proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., G
McGrath J., Seeburg P.H., Libermann T.A., Schlessi
Francke U., Levinson A., Ullrich A.;
"Tyrosine kinase receptor with extensive homology
shares chromosomal location with neu oncogene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-86118663; PubMed-3003577;
MEDLINE-87 Trans S., Aklyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P04626;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine surface receptor HER2) (MLN 19).
ERBB2 OR HER2 (NR NGL OR NEU.
                                       tyrosine phosphate.
                                                                       -!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE GF30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY E(F, TGF-ALPHA AND AMPHIREGULIN.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                              specific competition hybridization.";
Genomics 15:426-429(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-86070181; PubMed-2999974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyaj. Saito T., Toyoshima K.; Saito T., Toyoshima K.; "Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor."; Nature 319:230-234(1986).
                                                                                                                                                                                                                   Ehsani A., Low J., Wallace R.B., Wu A.M.; "Characterization of a new allele of the
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86016729; PubMed-2995967; Semba K., Kamata N., Toyoshima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 737-1031 FROM N.A.
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(POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
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CSF2_MOUSE
CSF2_FELCA
NUC2_RHIME
RL5_THME
RK12_NICSY
RK12_TOBAC
UREE_ALCEU
GIDB_COXBU
HAN1_SHEEP
                                         EACH
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                                         OF THE OTHER ERBB RECEPTORS
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Chen E., Gray A., Schlessinger

γ A., τ J.,

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EGF receptor

Nomura N., Miyajima

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Pfam; PF01030; Recep_L_domain;
Pfam; PF02757; YLP; 2.
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SMART; SM00261; FU; 3
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InterPro: IPR000719; Euk_pkinase.
InterPro: IPR002174; Furin-like.
InterPro: IPR001245; Tyr_pkinase.
InterPro: IPR004019; YLP_motif.
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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PS00109; PROTEIN_KINASE_TYR; 1.
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brane; Glycoprotein; Multigene f.
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   Y SIMILARITY.
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SIMILARITY).
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ATP-binding; Phosphorylation;
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Granulocyte-macrophage colony-stim
(Colony-stimulating factor) (CSF)
                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-85242684; PubMed-3925454;
Lee F., Yokota T., Otsuka T., Gem
Arai K.-I., Rennik D.;
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MEDLINE=86205844; PubMed=3486413
                                                                                       "Isolation of cDNA colony-stimulating
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hcmo.
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Cantrell M.A., Anderson D., Cerretti D.P., Price V., McKereghan K., Tushinski R.J., Mochizuki D.Y., Larsen A., Grabstein K., Cosman D.; "Cloning, sequence, and expression of a human granulocyte/macrophage colony-stimulating factor."; Proc. Natl. Acad. Sci. U.S.A. 82:6250-6254(1985).
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granulocyte-macrophage colony-stimulating
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*Structure of the chromosomal gene 
stimulating factor: comparison of t 
EMBO J. 4:2561-2568(1985).
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MEDLINE=92235844; PubMed=1569568;
Walter M.R., Cook W.J., Ealick S.E., N
                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE-92108420; PubMed-1837174;
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                                        ASTHMA.
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(Novartis). Used in myeloid reconstitution followir ransplant, bone marrow transplant engressis.
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           yeloid reconstitution following transplant engraftment failure
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Pfam; PF01109; GM_CSF; 1.
PRINTS; PR00693; GMCSFACTOR.
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EMBL; M11220; AAA52578.1; -.
EMBL; X03021; CAA26822.1; -.
EMBL; M10663; AAA52121.1; -.
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Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.
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         Pfam; pF00059; pkinase; 1.

R Pfam; pF00757; Furin-like; 1.

R Pfam; pF00757; Furin-like; 1.

R Pfam; pF00757; Furin-like; 1.

R Pfam; pF00757; YLP; 2.

R Pfam; pF002757; YLP; 2.

R Pfam; pF002757; YLP; 2.

R Pfam; pF00757; Furin-like; 1.

R Pf005075; SM00261; FU; 3.

R SMART; SM00219; Tyrkc; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

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Transferase; Tyrosine-protein; Multigene family; Receptor; Signature family; Phosphory

Transferase; Tyrosine-protein kinase; ATP-binding; Phosphory
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                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002145; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (pl85erbB2) (NEU proto-oncogene) (C-erbB-2).
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Q60553;
15-DEC-1998 (Rel.
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MEDLINE-94193007;
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Eukaryota; Metazoa; Chordata; Craniata
Mammalla; Eutheria; Rodentia; Sciurogn
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Yamazaki Y., Ishikawa T.;
"Cloning and activation of the Syrian
Gene 140:251-255(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH (POTENTIAL).
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jima <u>T</u>., Ishizaka Y., Nagao M., Arai
mutation
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Sciurognathi; Muridae;
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S PHOSPHORYLATION
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                     Phosphorylation;
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; Cricetinae;
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Matches
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P06494;

01-JAN-1988 (Rel. 06, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)

(p185crb2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth fareceptor-related protein).

ERBB2 OR NEU.

Rattus norvegicus (Rat).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SEQUENCE
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                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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RECEPTOR PROTEIN-TYROSINE
EXTRACELLULAR (POTENTIAL)
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SEQUENCE

FROM

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InterPro; IPRO00494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002174; Tyr_pkinase.
InterPro; IPR0021245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; YLP; 2.
Pfam; PF001001; Euk_pkinase; 1.
Pfam; PF001001; Euk_pkinase; 1.
SMART; SM00219; TyrKo; 1.
SMART; SM00219; TyrKo; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newman R., Crumpton M.J., Sternberg M.J.E., Campbell "Three dimensional structure of the transmembrane reg oncogenic and oncogenic forms of the neu protein."; EMBO J. 11:43-48(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "An extended family of protein-tyrosine kinase expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
    DOMAIN
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NP_BIND
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PIR; A24562; TVRTNU.
HSSP; P11362; 1FGK.
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MEDLINE-91222560;
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[2]
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MEDLINE-86118662; PubMed-3945311;
Bargmann C.I., Hung M.-C., Weinberg R.A.;
"The neu oncogene encodes an epidermal gr
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                                                                                                                                               Proto-oncogene;
                                                                                                                                                             Transferase;
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SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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                                                                                                                                                                                       PS00107; PROTEIN_KINASE_ATP; 1.
PS00109; PROTEIN_KINASE_TYR; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
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2155181; PubMed=1346763;
.J., Bottomley A.C., Lof
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                                                                                                                                                             Tyrosine-protein
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RECEPTOR PROTEIN-TYROSINE EXTRACELULAR (POTENTIAL). POTENTIAL). CYTOPLASMIC (POTENTIAL). CYS-RICH. CYS-RICH. CYS-RICH. ATP (BY SIMILARITY).
                                                                                                                                                        Multigene family; Receptor; Signal; n kinase; ATP-binding; Phosphorylation;
                                                                                                                             POTENTIAL.
                                                                                              PROTEIN-TYROSINE KINASE ERBB-2
LULAR (POTENTIAL)
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               reactive surface a phosphatase.";
J. Biol. Chem. 266:
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                                                                                                                                                                                                                                    MEDLINE=92272747; PubMed=1375464;
Sharilef F.S., Li S.S.-L.;
"Structure of human prostatic acid phosphatase gene.";
Biochem. Biophys. Res. Commun. 184:1468-1476(1992).
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Prostatic acid phosphatase precursor (EC 3.1.3.2).
                                                                          "Covalent structure,
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Biochem. Biophys.
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prostatic acid phosphatase.";
FEBS Lett. 236:275-281(1988).
                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Nucleotide sequence of human prostatic acid including seven Alu repeats.";
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"Structural origins of L(+)-tartrate
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MEDLINE-99023966; Pubmed-9804805;
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Blochem. Mol. Biol. Int. 33:561-565(1994).
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"Nucleotide sequence of human prostatic from a full-length cDNA clone.";
Nucleic Acids Res. 18:4928-4928(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90370491;
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MEDLINE-88312981;
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Biol. Chem. 273:30406-30409(1998).
Biol. Chem. 273:30406-30409(1998).
CATIVITY: An orthophosphoric monoester + H(2-2000) + phosphate.
SUBUNIT: HOMODIMER.
SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE
                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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ndan M.V., Patel P.C.;
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cDNA encoding human
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RESULT 6
CSF2_SHEEP
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Best Local
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Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Caprinae; Ov
NCBI_TaxID=9940;
                                                                                                                                                                                                                    CSF2_SHEEP
P28773;
"Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-stimulating factor.";
Gene 105:275-279(1991).
-i- FUNCTION: CYTOKINE THAT STIMULATES THE GROWTH AND DIFFERENTIATION OF HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES (BY
                                                                                                                                                      01-DEC-1992 (Rel. 24, Createw, 01-DEC-1992 (Rel. 24, Last sequence update) 01-DEC-1992 (Rel. 24, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) Granulocyte-macrophage colony-stimulating factor (CSF).
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MEDLINE-92039044; PubMed-1937025;
MCInnes C.J., Halg M.C.K.;
"Cloning and expression of a cDNA"
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CONFLICT
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SIGNAL
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Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; 3D-structure.
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; S11147; S11147.
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35; Conserv
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GEGOLTOL -> RIWPTHPA (IN R
E -> D (IN REF. 3).
A -> R (IN REF. 5).
O -> R (IN REF. 5).
P -> A (IN REF. 5).
P -> A (IN REF. 3).
C -> V (IN REF. 3).
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Pred. No. 8.9
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N-LINKED (GLCNAC.
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Matches 22
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P70424; Q61525;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbs-2 (EC 2
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protein, ARIA/heregulin, and its putative receptors, ErbB2 in developing mammalian muscle.";
Dev. Biol. 172:158-169(1995).
-i- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EG
                                                                                                                    Lim J., Dey S.K., Das S.K.;
"Differential expression of the erbB2 gene in mouse uterus: potential mediator of signaling factor-like growth factors.";
Endocrinology 138:1328-1337(1997).
                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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pfam; pF01109; GM_CSF; 1.
pRINTS; PR00693; GMCSFACTOR.
proDom; pD007349; GM_CSF; 1.
smart; SM00040; CSF2; 1.
                                                                              SEQUENCE OF 150-245 FROM N.A. MEDLINE-96069911; PubMed-7589796; MOSCOSO L.M., Chu G.C., Gautam M.,
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HSSP; P04141; 2GMF.
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                                                                        Sanes J.R.;
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                                                           Synapse-associated expression of an
                                                                                                                                                                        MEDLINE=97200814; PubMed=9048643;
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SUBUNIT: MONOMER (BY SIMILARITY).
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Rodentia;
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N-LINKED (GLCNAC
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1.4e-13;
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SP30 IS A
SGF, TGF-
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CSF2_CAVPO
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Matches 20
                                                  Olynoval, (1904) (Rel. 35, Created) Ol-NOV-1997 (Rel. 35, Last sequence update) Ol-NOV-1997 (Rel. 35, Last annotation update) Ol-NOV-1997 (Rel. 35, Last annotation update) Granulocyte-macrophage colony-stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
NON_CONS
NON_TER
SEQUENCE
                                                                                                                                                                 CSF2_CAVPO
Q60481;
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-i- TISSUE SPECIFICITY: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                            CSF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PROO109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U71126; AAB17380.1;
EMBL; L47239; AAA93532.1;
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iransmembrane; Glycoprotein; Multigene family; Receptor; Transferase;
                                                                                                                                                                                                                                                                                            210
                                                                                                                                                                                                                                                                                                                 363 PRSPLAPSEGAGSDVFDGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: ON DAYS 1-4 OF PREGNANCY, ERBB2 IS DETECTE PRIMARILY IN EPITHELIAL CELLS, THE DAY I THERUS SHOWING THE PRIMARILY IN EPITHELIAL CELLS, THE DAY I THERUS SHOWING THE HIGHEST ACCUMULATION, ON DAY 5, THE EPITHELIUM AND THE EMPLANTING BLASTOCYST EXHLBIT ACCUMULATION OF THIS RECEPTOR. ON DAYS 6-8, THE EXPRESS IN THE EFITHELIUM AT BOTH THE IMPLANTATION AND INTERIMPLANTATION SITES IN ADDITION TO MODEST LEVELS IN THE EXPRESS SECONDARY DECIDUAL ZONE. ON DAYS 7 AND 8, ACCUMULATION IS ALSO PROMINENT IN THE TROPHOBLASTIC GIANT CELLS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY). REFORE PROFIDER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA AND AMPHIREGULIN.
CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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245
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EXPRESSED PREDOMINANTLY IN UTERINE EPITHELIAL
EXPRESSED PREDOMINANTLY TO THE SYNAPTIC SITES
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Pred. No.
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  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                    PRT;
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RESULT 9
CSF2_CANFA
ID CSF2_C
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DT 01-FEB
DT 01-FEB
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DE Granul
DE (Colon
GN CSF2.
OS CANIS
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Best Local
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01-FEB-1996
01-OCT-1996
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Yuan H.T., Kelly F.J., Bingle C.D.;
Yuan H.T., Kelly F.J., Bingle C.D.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: CYTOKINE THAT STIMULATES THE GROWTH AND DIFFERENTIATION
OF HEMATOPOLETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING
OF HEMATOPOLETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING
                         MEDLINE-91329842; PubMed-1868252; Mash R.A., Schuening F., Appelbaum F., Han Morris C.F., Slichter S.J., Storb R.; "Molecular cloning and in vivo evaluation macrophage colony-stimulating factor.";
                                                                                                                                                                                  CSF2_CANFA
P48749;
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NON_TER
SEQUENCE
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DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                    Granulocyte-macrophage colo (Colony-stimulating factor)
                                                                        SEQUENCE FROM N.A.
                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                      Canis familiaris
                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                               Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000773; GM_CSF.
Pfam; PF01109; GM_CSF; 1.
ProDom; PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U46779; AAA87592.1; -. HSSP; P04141; 2GMF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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NCBI_TaxID=10141;
[1]
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ophage (1997) of 78:930-937(1991).
FUNCTION: CYTOKINE THAT STI
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        Growth factor;
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                                                                                                                                                                                                                                                                                                         140
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zoa; Chordata; C
cia; Carnivora;
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e colony-stimulating f
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  STIMULATES THE SOR CELLS FROM V
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Pred. No.
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N-LINKED
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GRANULOCYTE-MACROPHAGE
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                                                       Hammond
                                                                                                          Vertebrata;
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7e-05;
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  E GROWTH
VARIOUS
                                      of
                                                                                                                                              factor
                                                                                                    Canidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                     canine
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                                                        W.P.,
                                                                                                                                                                                                                                                                                      Length 140
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                                                                                                                                              precursor (GM-CSF)
  AND DIFFERENTIATION LINEAGES, INCLUDING
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) (POTENTIAL)
                                    granulocyte.
                                                                                                    Canis
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RESULT 10
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Best Local
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or send a
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DISULFID
CARBOHYD
SEQUENCE
                                                                                                           This
                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update Granulocyte-macrophage colony-stimulating f. (Colony-stimulating factor) (CSF).
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P51748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine;
SIGNAL
                                                                                                                                                                        Submitted (SEP-1994) to the EMI-i- FUNCTION: CYTOKINE THAT STORED OF HEMATOPOIETIC PRECURSOR
                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
Cervidae; Cervinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01109; GM_CSF; 1.
PRINTS; PR00693; GMCSFACTOR.
ProDom; PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
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                                                                                                                                                                                                            SEQUENCE FROM Lockhart E.A.;
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                                                                                                                                                                                                                                                                                                Cervus elaphus (Red
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                                                                                               SWISS-PROT entry is copyright.
een the Swiss Institute of Bio
                                                                                                                                                           GRANULOCYTES, MACROPHAGES,
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U14392;
P04141;
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                                  equires a license agreement ( email to license@isb-sib.ch)
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actyla; Ruminantia;
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209118; Q29046; O1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation)
                   EMBL;
                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           Gloster S. Submitted
                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                   SUBUNIT: MONOMER.
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FUCCTION: CYTOKINE THAT STIMULATES THE GROWTH AND DIFFERENTIATION OF HEMATOPOLETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES (BY
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Best Local
                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=90021093; PubMed=2678728;

Leong S.R., Flaggs G.M., Lawman M.J.P., Gray P.W.;

Colony-stimulating factor.";

Vet. Immunol. Immunopathol. 21:261-278 (1989).

1-- FUNCTION: CYTOKINE THAT STIMULATES THE GROWTH AND DIFFERENTIATION OF HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING OF HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, EDSINOPHILS AND ERYTHROCYTES (BY
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SIGNAL
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SEQUENCE FROM N.A.

MEDILINE-89096971; Pubmed-3062386;

Maliszewski C.R., Schoenborn M.A., Cerretti D.P.,

Maliszewski C.R., Schoenborn M.A., Gillis S.,

Picha K.S., Cosman D., Tushinski R.J., Gillis S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pii052;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01109; GM_CSF; 1.
PRINTS; PR00693; GMCSFACTOR.
ProDom; PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
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Cytokine; Growth factor; Gl
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                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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Baker P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor (GM-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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of the
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                                                                                collaboration
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license@isb-sib.ch).

(See http://www.isb-sib.ch/announce,

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Best Local s
Matches 10
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PIR; JL0037; FQBCGM.
HSSP; P04141; 2GMF.
InterPro; IPR000773; GM_CSF.
Pfam; PF01109; GM_CSF; I.
PRINTS; PR00693; GMCSFACTOR.
Pr0D0m; PD007349; GM_CSF; I.
                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998
15-JUL-1998
16-OCT-2001
Zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                        Alc2.
Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
Aboria; Rodentia;
                                      EMBL; D70848; BAA11115.1;
HSSP; P08047; 1SP2.
TRANSFAC; T04670; -.
MGD; MGI:106679; Zic2.
                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                          use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                  This
                                                                                                                                                                                                                             gene
                    MGD; MGI:106679; zic2.
InterPro; IPR000822; zni
Pfam; PF00096; zf-C2H2;
                                                                                                                              the
                                                                                                                                                                                                                                              Aruga J., Nagai T., Tokuyama
Chapman V.M., Mikoshiba K.;
                                                                                                                                                                                                                                                                  TISSUE-Cerebellum;
MEDLINE-96132843; PubMed-8557628;
                                                                                                                                                                                                                                                                                                                                                                                               062520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine; Growth factor; Glycoprotein; Signal SIGNAL 1 17
          PRINTS;
                                                                                                                                         between
                                                                                                                                                                                                -1- SUBCELLULAR LOCATION:
-1- TISSUE SPECIFICITY: CI
                                                                                                                                                                                                                    J. Biol.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        ZIC2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598
                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Buropean Bioinformatics Institute. There are no restricted in the swiss institute as a long as its content
                                                                                                                                                                     PROTEINS.
                                                                                                                                                                            SIMILARITY: BELONGS TO THE GLI FAMILY
                                                                                                                                                                                       CEREBELLUM.
                                                                                                                                                                                                                mouse zic gene family. Homologues odd-paired."; 101. Chem. 271:1043-1047(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEPTCLQTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEPTCLQTRL
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10; Conser
            PR00048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400040; CSF2;
PS00702; GM_4
                                                                                                                                                                                                                                                                                                                                                      (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation updat
protein ZIC2 (Zinc finger prote
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104
44
54
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ZINCFINGER.
; Znf_C2H2;
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137
44
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                             Znf_C2H2.
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Pred. No.
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                                                                                                                                                                                                           lear.
                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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protein
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                                                                                                                                                                                                                                                         Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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                                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                        cerebellum
                                                                                                                            restrictions
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                                                                                                          and
                                                                                                                                                                                                 SEEN
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ZIC2_HUMAN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                    stengel-Rutkowski S., Hennekam R.C., M. "Holoprosencephaly due to mutations in odd-paired.";
EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
ZN_FING
ZN_FING
ZN_FING
DOMAIN
                                      the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.lsb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     TISSUE-Brain;
MEDLINE-20556339; PubMed-10984499;
Yang Y., Hwang C.K., Junn E., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                   -i- SUBCELLULAR LOCATION: Nuclear.

-i- DISEASE: DEFECTS IN ZIC2 ARE A CAUSE OF HOLOPROSENCEPHALY TYPE
(HPES), HPES IS A STRUCTURAL ANOMALY OF THE BRAIN.

-i- SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                           "ZIC2 and Sp3 repress Sp1-induced act receptor gene.";
J. Biol. Chem. 275:38863-38869(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIC2_HUMAN
095409; Q9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger;
                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
MEDLINE=98442655; Pu
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger protein ZIC2 (Zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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AF104902; AAC96325.1;
AF193855; AAG28409.1;
P08047; 1SP2.
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97
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239
415
327
357
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367
512
55492
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                                                                                                                                                                                                                                                                                            PubMed=9771712;
rton D., Brown L.Y.,
S., Hennekam R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC_FINGER_C2H2_1; 3.
ZINC_FINGER_C2H2_2; 4.
l-binding; DNA-binding;
POLY-HIS.
                                                                                                                                                                                                                                                                                                                           AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%;
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POLY-ALA.
POLY-HIS.
ZINC FINGERS.
C2H2-TYPE (A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9; 1
Pred. No.
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0065BD75B52E7DD2 CRC64;...
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                                                                                                                                                                                                  activation
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in ZIC2,
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                                                                                                                                                                                                                                                                                a homologue of Drosophila
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                                                                                                                                                                                                                                                                                                        Roeder
                                                                                                                                                                                                                                                                                                                                                                                                  the cerebellum
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                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                          HOTIO
                                                                                  restrictions
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                                                                                                     collaboration
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                                                              in no way commercial
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TRANSFAC; T04237;

collaboration outstation

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RESULT 15

REGER_CHICK
ID REGER_C
AC P13387
DT 01-JAN
DT 15-JUN
DT 01-JEN
CO ELWARY
OC ELWARY
OC AICHOS
OC GALLUS
OX NCBLLI
RN (1]
RN (1]
RN (1]
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RN (1)
RT EXPUE
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Best Local S
Matches 9
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P1387: 01-JAN-1990 (Rel.
01-JAN-1990 (Rel.
15-JUN-2002 (Rel.
15-JUN-2002 (Rel.
Epidermal growth)
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SEQUENCE
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ZN_FING
ZN_FING
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DOMAIN
DOMAIN
                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000003; Znf_C2H2; 1.
SMART; SM00355; ZnF_C2H2; 4.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-88261272; PubMed-3260329;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
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MIM; 603073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
                 tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLABOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complinduction of the tyrosine kinase activity, stimulation synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ааанннннн
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9; Conser
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532
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(Rel. 13, Last sequence update)
(Rel. 41, Last annotation update)
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llarity 100.0%;
Conservative
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226
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sp_bacteria:*
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sp_mhc:*
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       Q8WYV0
Q9BG5
Q18735
Q9GL44
Q9GM0
Q96GM0
Q96GM0
Q8RZXI
Q9KK4
Q96KK4
Q96KK4
Q95U10
Q95U10
Q8S7E3
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Q14256
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O9g144 macaca mula
O96ky0 homo saplen
O96gm0 homo saplen
O96gm0 homo saplen
O8r2x1 mus musculu
O9myk4 ovis aries
O96gk9 homo saplen
O8wn17 equus cabal
O95110 equus cabal
O95191 marmota mon
O8xu41 ralstonia s
O8x723 oryza sativ
                                                                                                                                                                                                                                                                        Q9uk79
Q14256
Q8wyv0
Q9bg66
Q18735
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Q9FRB3	Q9A8Z2	Q9VUD9	Q98GZ5	Q97S36	Q9I072	Q9ASW4	Q8R1J9	Q9LU37	Q8S723	Q8S3R4	Q9R640	Q9D4 I5	Q8Y325	Q9AXB3	Q8XX14	Q9XE33	Q94 IM0	000837	Q8R5B5	Q9EP98	Q9QX70	096680	Q9VML1	Q9WVF5	Q9ERV6	Q9PSH2	Q90836	Q9ESE0	
	Q9a8z2 caulobacter	Q9vud9 drosophila	Q98gz5 rhizobium l	Q97s36 streptococc	Q\$1072 pseudomonas	Q9asw4 arabidopsis	Q8r1j9 mus musculu	arab		Q8s3r4 oryza sativ	Q9r640 mycobacteri		Ο.	Q9axb3 oryza sativ	Ç8xx14 ralstonia s		0	000837 leishmania	Q0r5b5 mus musculu	09e⊱98 mus musculu	Q9qx70 rattus norv	0		€9wvf5 mus musculu	mus mus	gall	0836 gallus		

ALIGNMENTS

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Best Local :
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SEQUENCE FROM N.A.

MEDLINE=94000386; PubMed=8104414;

Sarkar F.H., Ball D.E., L1 Y.W., C

Sarkar F.H., Ball D.E., L1 Y.W., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q14256;
Q14256;
                 Q8WYV0;
01-MAR-2002
                                      Q8WYV0
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-86070181; PubMed-2999974;

MEDUNE-86070181; PubMed-2999974;

Coussens L., Yang-Feng T.L., Liao Y.C., Che
Seeburg P.H., Libermann T.A., Schlessinger
Levinson A., Ullrich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-erb B2/neu
C-ERB B2.
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                                                                                                                                                                                                                                                                                                                                                                            "Tyrosine kinase receptor with extensive homology shares chromosomal location with neu oncogene.";
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L; M95667; AAC37531.1; -.
                                                                                         GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAEN
                                                                                                                                                                           CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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                                                                                                                                                                                                                      165;
                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                             165 AA;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                      Conservative
                                       PRELIMINARY;
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                  20,
                  Created)
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Pred. No.
                                      PRT;
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                                                                                                                                                                                                                      Mismatches
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g of an intron
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J., Francke U.,
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Matches 132; Conserv
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Hypothetical 44.7 kDa protein
PP3659.
                                                                                                                 "ErbB genes and epidermal growth factor- (EGF-) peri-implantation rabbit uterus and blastocyst. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ d EMBL; AF333178; AAK14371.1; -
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Klonisch T., Wolf P.,
Tetens F., Fischer B.;
                                                                    Kinase
                                                                                                                                                                                                                                                                                                                                                                                       Receptor tyrosine kinase ErbB2 (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vei
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Novel human cDNA clones with function growth.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pfam; PF00069; pkinase; 1.
Pfam; PF02757; YLP; 2.
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EMBL; AF318349; AAL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huang Y., Zhou X.M.,
Wan D.F., Gu J.R.;
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 412 AA; 4
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InterPro; IPR000719;
InterPro; IPR001245;
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AAL55856.1;
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YLP_motif.
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       7CB3792A54FC49BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Leporidae;
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                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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RESULT
Q9GL44
ID Q9GL40
AC Q0
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DT 00
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Best Local S
Matches 67
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Best Local
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                             PRODOM; FULL 3.

SMART; SM00261; FU; 3.

SMART; SM00219; TYPRC; 1.

SMART; SM00219; EF_HAND; UNKNOWN_1.

PROSITE; PS000107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

ATP-binding; Transferase; Tyrosine-protein kinase.

ATP-binding; Transferase; Tyrosine-protein kinase.
 Q9GL44
Q9GL44;
Q1-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00757; Furin-like; 1. pfam; PF00069; pkinase; 1. pfam; PF01039; Recep_L_domain; Pfam; PF02757; YLP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1997)
EMBL; AB008451; BAA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         018735;
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                                                                                                                                    311 GASCVT 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT :309
                                                                                                              GASCVT
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                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002174; Furin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000494; EGFR_L_domain
IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                            IPR004019;
                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001245;
 l (TrEMBLiel.
l (TrEMBLiel.
l (TrEMBLiel.
                                                                                                              297
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llarity 100.0%;
Conservative
                                                                                                                                                                                                              Conservative
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                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of erbB-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAA23127.1;
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                                                                                                                                                                                                                                        9.68;
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21,
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EMBL/GenBank/DDBJ databa
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                           Created)
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                                                                                                                                                                                                                           Score 66;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cranlata; Vertebrata;
; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                      DB 6;
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Canis.
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Q96KY0
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Best Local S
Matches 35
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Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted (AUG-2000) to the EMBL/GenBank/DDBJ day
EMBL; AY007376; AAG16626.1; -
HSSP; PO4141; ZGME,
InterPro; IPR000773; GM_CSF.
Pfam; PF01109; GM_CSF; 1.
PRINTS; PR00693; GMCSPACTOR.
PrODom; PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
PROSITE; PS00702; GM_CSF; 1.
PROSITE; PS00702; GM_CSF; 1.
PARSIANT 60 60 V -> I.
Q96QM0 PRELIMINARY;
Q96QM0;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hutchinson K.L., Villinger F., Miranda M.E., Peters C.J., Rollin P.E.; "Multiplex analysis of cytokines in the sera
                                                                                                                                                                                              InterPro: IPR000560; Hisac_phsphtse.
Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
SEQUENCE 386 AA; 44540 MW; FE90E10CEBECADEA CRC64;
                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; BC016344; AAH16344.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TREMBLIEL 19, 01-DEC-2001 (TREMBLIEL 19, 01-MAR-2002 (TREMBLIEL 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96KY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Granulocyte-macrophage colony-stimulating factor
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-PROSTATE;
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                          Acid phosphatase, prostate. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q96КY0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
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36; Conserv
                                                                                                                                                   35; Conser
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ilarity 100.0%;
Conservative
                                                                                                                                                5.1%; S
llarity 100.0%;
Conservative 0;
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                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                   Primates;
                                                                                                                                                                                                                                                                                                                                                              Chordata;
  19,
19,
                                                                                                                                                Score 35; DB 4; Pred. No. 1.3e-; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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7D5F381DA2FC832F CRC64;
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Matches
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InterPro; IPR000560; HisAc_phsphtse.

Pfam; pf00328; acid_phosphat; 1

PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.

SPONIENCE 418 AA; 48308 MW; 68E10406974E4462 CI
                                                                                           Ovis aries (Sheep).

Gukaryota; Metazoa; Chordata; Craniata;
Mammalla; Eutheria; Cetartiodactyla; Run
Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                                                                                                                                                                       O9MYK4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-DEC-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TIEMBLIEL 21, CI
01-JUN-2002 (TIEMBLIEL 21, La
01-JUN-2002 (TIEMBLIEL 21, La
Hypothetical 40.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strauberg R.;
Submitted (ApR-2002) to the EMBL; BC027080; AAH27080.1;
Hypothetical protein.
SEQUENCE 367 AA; 40163 M
  O'Brien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                        SEQUENCE FROM N.A. MEDLINE-91331592;
                                                                                                                                                                                                               Granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                           Q9MYK4
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8R2X1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Homo sapiens (Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PROSTATE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463
                                                                                                                                                                                                                                                                                                                                                                                                                                                               283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 3.9%; Score 27;
Similarity 100.0%; Pred. No.
27; Conservative 0; Mismatc
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35; Conserv
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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       Rothel
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                           PubMed-1869289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40163 MW;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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  H.F.,
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                                                                                                                                               Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                        144
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  Mood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; 1
1.7e-18;
                                                                                                                                                                Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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; Murinae; Mus
                                                                                                                                                                     Euteleostomi;
                                                                                                                                               Bovoidea;
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Q8WN17
  RAA
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Best Local S
Matches 20
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Best Local S
Matches 22
                                                                                                                                                              QBWN17;
QBWN17;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Granulocyte-macrophage colony-stimulating factor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PFO PROSITE; PROSITE;
Vecchione
Catchpole
                                                                                         Equus caballus (Horse).
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9796;
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                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                        Q8WN17
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PRELIMINARY;

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Kanellos

T.S.,

Howard

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Hamblin

A.S.

Euteleostomi;

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EMBL; X55991; CAA39463.1; -. HSSP; P04141; 2GMF.
InterPro; IPR000773; GM_CSF.
Pfam; PF01109; GM_CSF; 1.
PRINTS; PR00693; GM_CSF, 1.
PRODOM; PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00702; GM_CSF; 1.
NON_TER 144 144
SEQUENCE 144 AA; 16290 MW
                                                                                                                                                                                 Strausberg R;
Submitted (MAY-2001) to the EMBL/Gen
EMBL; BC008493; AAH08493.1; -.
InterPro; IPR000560; Hisac_phsphtse.
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and sequencing of the cDNA for colony stimulating factor (GM-CSF)."; Immunol. Cell Biol. 69:51-55(1991).
                                                                                                                                                                                                                                               TISSUE-PROSTATE;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Acid phosphatase, pr
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                           NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598 QEPTCLQTRLELYKQGLRGSLT
            16 LGFLFLLFFWLDRSVLAKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEPTCLQTRLELYKQGLRGSLT
LGFLFLLFFWLDRSVLAKEL
                                                                                                       Pr00328; acid_phosphat; 1.

Pr00328; acid_phosphat; 1.

TE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.

TE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.

44515 MW; A4D817CECIDCIA84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
22; Conserv
                                                                           Similarity
                                                        2.9%;
nilarity 100.0%;
Conservative 0
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Primates;
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Last annotation update)
                                                                          Score 20;
Pred. No.
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Catarrhini;
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                                                           Mismatches
                                                                          DB 4; L:
2.4e-11;
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8.6e-14;
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i; Hominidae;
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                                                                                      Length 386;
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PRINTS; PR00693; GMCSFACTOR.

PRODOM; PD007349; GM_CSF; 1.

SMART; SM00040; CSF2; 1.

PROSITE; PS00702; GM_CSF; UNKNOWN_1.

NON_TER 146 146

SEQUENCE 146 AA; 16594 MW; 162C191
                                                                                            099991 PRELIMINARY; PRT; 138 AA.
099J91;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Granulocyte-macrophage colony stimulating factor precursor.
Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q95L10
Q95L10;
SEQUENCE FROM N.A. Wu H.-L., Chen P.-J., "Molecular Cloning an
                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                      Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY040203; AAK72108.2; -
EMBL; AY040203; AAK72108.2; -
InterPro; IPR000773; GM_CSF.
Pfam; PF01109; GM_CSF; 1.
Probom; PD007349; GM_CSF; 1.
PROSSITE; PS00702; GM_CSF; UNKNOWN_1.
SEQUENCE 152 AA; 17173 MW; 75605CC1ADE9EFE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Granulocyte-macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "cDNA for equine GM-CSF.";
Submitted (NOV-2001) to the
EMBL; AF448481; AAL41017.1;
                                                NCBI_TaxID=9995;
                                                             Marmota.
                                                                       Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                      Mauei S., Commandeur U., Steinbach F.;
"Cloning of equine granulocyte-macrophage
(eq.GM-CSF).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                             GPLTMMASHYKOHCPPT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conserv
                                                                                                                                                                                                                                                                          l Similarity
17; Conserv
                                                                      Eutheria;
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__urity 100.0%;
Conservative ^
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_arity 100.0%;
Conservative ^
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  and
                                                                       Chordata;
Rodentia;
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 Lin H.-K., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19, Last sequence update)20, Last annotation update)colony-stimulating-factor.
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19,
20,
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Pred. No.
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Pred. No.
                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Sciuridae; Sciurinae;
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 Lee
n of
R.-S., Lin H.-L., Chen D.-S.; Woodchuck Granulocyte-Macrophage
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                                                                                                                                                                                                                                                                                      1.1e-08;
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                                                                                                                                                                                                                                                                                                Length 152
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Pfam; PF01109; GM_CSF; 1.
PRINTS; PR00693; GMCSFACTOR.
PRODOm; PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
PROSITE; PS00702; GM_CSF; 1.
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Ol-MAR-2002 (TrEMBLrel. 20, Created)
Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Ol-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Hypothetical transmembrane protein RSc3353.
RSC3353 OR RSO2628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal
SIGNAL
                                                                                                 Salanoubat M., Génin S., Artiguenave F., Gouzy J., Mangenot S
Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L.,
Chaine N., Choisne N., Claudel-Renard C., Cunnac S., Demang
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum
Nature 415:497-502(2002).
EMBL; AL646074; CAD17141.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colony Stimulating Factor.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF255734; AAG49541.1; -.
EMBL; AF255735; AAG49542.1; -.
EMBL; P04141; ZGMF.
                                                                                          Hypothetical protein; SEQUENCE 253 AA; 2
                                                                                                                                                                                                                                                                                        Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; beta subdivision; Ralst
                                                                                                                                                                                                                                                                                                                                                                                    Q8XU41
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                                                                                                                                                                                                                     MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                 STRAIN-GMI1000;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              Ralstonia
                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                 NCBI_TaxID=305;
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                                             Conservative
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/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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US-08-447-083-68
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US-08-469-318-193-2
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US-08-469-318-160
US-08-468-699-160
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TOPOLLOGY: unknown
MOLECULE TYPE: polypeptide
SEQUENCE DESCRIPTION: SEQ 1
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                                                                                 Query Match
Best Local Sim
Matches 292;
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Patent No. 6414130
GENERAL INFORMATION:
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 206 628-7621
TELEPAS: 206 628-7699
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                          38 GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ
 98 EVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLR 157
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/630,155
FILING DATE: 16-Jan-2001
CLASSIFICATION: CUDKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: DAVISON, BAITY L.
REGISTRATION NUMBER: 47,309
REFERENCE/DOCKET NUMBER: 49321-10
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: Windows95
SOFTWARE: WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Doherty, Joni Kristin and Gail M. TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVIS WRIGHT TREMAINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                             GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                          LENGTH: 419
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US-08-469-318-141

US-08-468-609A-141

US-08-468-609A-141

US-08-762-227A-141

PCT-US95-01185-144

US-08-468-609A-144

US-08-468-609A-144

US-08-468-672A-144

US-08-468-672A-144

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Patent No.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERNTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                          MOLECULE TYPE: PI
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                    ORGANISM: homo saplens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig.
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                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09, FILING DATE: 03-SEPT-1998
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EVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLR 157
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Similarity 100.0%; Pred. No. 3.5e-269;
92; Conservative 0; Mismatches 0;
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Ruegg, Curtis L.
Wu, Hongyu
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                                                                                                                                       Length 782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,823A
FILING DATE: 03-DEC-1998
CILASSEPICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08579823A Patent No. 6080409
                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-324-081
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wu, Hongyu
139
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                                                                                    98
                                                                                                                                                                                                                                                                                                                               LENGTH: 782 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                         Match 42.3%; Score 292; DB 3; Local Similarity 100.0%; Pred. No. 3.5e-269; es 292; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                    EVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLR 157
                         ELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPM 217
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                                                                                                                                                                                                                                                GM-CSF-Her-2 fusion protein; Fig.
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Best Local
                                                                                                                                                                                    Matches 292;
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                                                                       98
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                                                                                                                              38 GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ 97
                                                                                                                                                                                                       Local Similarity
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NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 76
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ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT
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TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                    EVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLR 157
ELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPM
                                                                                                          GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ
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                                    EVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLR
                                                                                                                                                                                                                                                                         ONAL SOCIAL INDIVIDUAL ISOLATE: GM-CSF-Her-2 INDIVIDUAL ISOLATE: GM-CSF-Her-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/344,195 FILING DATE: 24-Jun-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/146,283 FILING DATE: 03-SEPT-1998
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Pred. No. 3.
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
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                                                    158 ELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNK:RACHPCSPM 217
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                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
                                                                                                    EVQGYVLIAHNQVRQVPLQRLRIVRGTQLEEDNYALAVLDNGDPLNNTTPVTGASPGGLR 157
                                                                                                                                                                      GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                       42.3%; Score 292; Di
100.0%; Pred. No. 5.1
:ive 0; Mismatches
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92:
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                                                                                                              ELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPM
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682-6031
NO: 68:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/981,165 FILING DATE: 24-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
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SOFTWARE: Patentin Release #1.0,
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                                                                                                                                          GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ
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Culouscou, Jean-Michel
Shoyab, Mohammed
Siegall, Clay B.
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SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No. 5.5e-269;
/ative 0; Mismatches 0;
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Best Local Similarity
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COUNTRY:
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PC-DOS/MS-DOS
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LENGTH: 1255 amino aci
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Disis, Mary L.
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REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
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RESULT 9
US-08-625-101-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sharkey, Richard G. REGISTRATION NUMBER: 32,629 REFERENCE/DOCKET NUMBER: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 01-APR-1996 CLASSIFICATION: 424
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                                 NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                                                       CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
                                                                                          CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCCHEQCAAGCTGPKHSDCLACLHF
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100.0%; Pr
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                                                                            Sequence 2, Application US/08356786 Patent No. 5877305
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Best Local Similarity
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                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
APPLICANT:
                              APPLICANT:
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MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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98104-7092
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Huston, James S.
Oppermann, Hermann
Houston, L. L.
Ring, David B.
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NO: 68:
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100.0%; Pred. No. 5.5e-269;
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US-08-466-680B-68

sequence 68, Application US/08466680B Patent No. 6075122 GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Biosynthetic Binding Protein TITLE OF INVENTION: Marker NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz,
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino aci
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 310
                NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                                                             CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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                                                            CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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5.5e-269;
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CORRESPONDENCE ADDRESS:

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Seed and Berry LLP

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                                                                                                                                                                                                                                                                                  JS-08-422-108-1
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Best Local Similarity
                                                                                                                                                                                                                                                              Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-631
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                             SENERAL INFORMATION:
                                                                                                                                                                                                                                              tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                            APPLICANT:
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OMPUTER READABLE FORM:
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                                               STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ 78
                  COUNTRY: U
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 277
                                                                                                                                                                                                                                                                                                                                                                      NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHPCSPM 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLR 157
                                                                                                                                                                                                                                                                                                                                                      NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 310
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                                                                                                                                                      Hudziak, Robert M.
Shepard, H. Michael
Ullrich, Axel
VENTION: HER2 EXTRACELLULAR DOMAIN
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SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No.. 5.
tive 0; Mismatches
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Sequence 1, Application US/08422734 Patent No. 6333169

GENERAL INFORMATION:

APPLICANT:

Hudziak,

Robert M.

APPLICANT: TITLE OF

Shepard, H. Michael Ullrich, Axel

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

INVENTION: HER2 EXTRACELLULAR DOMAIN

ADDRESSEE:

CITY: STREET:

SEE: Genentech, Inc. : 460 Point San Bruno Blvd South San Francisco California

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RESULT 14
US-08-422-734-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                              41 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
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                                                                GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 289
                                                                                               GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                                                                                                                                 SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
                                                                                                                                                                                                                                                                GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ
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                                                                                                                                                                                                 LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG
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Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee, Wendy M
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415/952-9881
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Pred. No.
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160 60 100

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120

220

280 180

SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS WinPatin (Genentech)

OPERATING SYSTEM:

COMPUTER READAL MEDIUM TYPE:

READABLE FORM: TYPE: 3.5 inc

inch, 1.44 Mb floppy disk

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                                                                                                                                  Patent No.
                                                                                                                                       Sequence 69, Application US/08414417B Patent No. 5801005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                     GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/422108
APPLICATION NUMBER: 08/355460
                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/31 FILING DATE: 13-DEC-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         281 GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/0 FILING DATE: 15-APR-1993
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                                                                                                                                                                                                                                                                                                                            SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
                                                                                                                                                                                                                                                                                                                                                                                           LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG 220
                                                                                                                                                                                                                                        GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 289
                                                                                                                                                                                                                                                                                                                                                                          LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG
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                                                                                                                                                                                                                                                                                                         SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee, Wendy
                                                                                Cheever, Martin A.
Disis, Mary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1989
                            IMMUNE REACTIVITY TO HER-2/neu PROTEIN
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.9%; Score 289; DB 4; L
100.0%; Pred. No. 2e-266;
O. Mismatches 0;
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Search completed: April 28, 2003, 13:46:38 Job time : 19 secs

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Best Local Similarity
                                                                                                                                                                                            Matches 132;
                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Sharkey, Richard G.
 483
                                                                423
                                                                                                                                           330 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLCMGAAKG 389
                                                                                            390 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 449
                                                                                                                              363 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG 422
                                                                                                                                                                                                                                                                          TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 31-MAI CLASSIFICATION: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
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STREET: 63
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PAARPAGATLER 461
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SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No. 4.1e-117;
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length: 2000000000
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690
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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US-09-821-883-1
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65	19	68	22	32	386	386	386	171	1256	293	1260	1256	654	135	610	144	127	127	127	600	589	587	583	266	191	
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US-09-466-320-12	US-09-466-320-20	US-09-466-320-11	US-09-466-320-19	US-09-821-883-11	US-09-822-827-945	US-09-974-546-48	US-09-895-793-945	US-09-925-300-1025	US-09-854-356-14	US-10-102-806-583	US-09-870-759-118	US-09-854-356-2	US-09-854-356-8	US-09-925-301-1232	US-09-783-708-1	US-09-923-246-114	US-09-800-016-1	US-09-821-883-18	US-09-792-793A-15	US-09-930-125-11	-09-930-125-	US-09-930-125-8	-930-125-	-05	US-09-441-411-9	
Sequence 12, Appl			Sequence 19, Appl	~	Seguence 945, App	Sequence 48, Appl	Sequence 945, App	Sequence 1025, Ap	Sequence 14, Appl	•	Sequence 118, App	Sequence 2, Appli	Sequence 8, Appl1	Sequence 1232, Ap	1, Ap	Sequence 114, App	Sequence 1, Appli	sequence 18, Appl	Sequence 15, Appl:		10,	•	Sequence 9, Appli	•	Sequence 9, Appli	

ALIGNMENTS

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; TYPE: PRT; ORGANISM: Artificial Sequence; FEATURE; OTHER INFORMATION: HER500-hGM-CSF construct US-09-821-883-2
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                                                                                                                                                                                                                                            Matches 690;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09821883 Patent No. US20020061310A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/193,504 PRIOR FILING DATE: 2000-03-30 NUMBER OF SEQ ID NOS: 30
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                                CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
                                                                                                      HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI
                                                                                                                     HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI
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Matches 549
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TYPE: PRT
ORGANISM: Artificial S
FEATURE:
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                                                                                                                                                                                                                                                                                        APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FBStSEQ for Windows Version 4.0
SEQ ID NO. 1
                                                                                                                                                     OTHER INFORMATION: HER500 construct
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49; Conservative
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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                                                                                                                                                                      Matches
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APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
                                                                                                                                                                                                                                                       LENGTH: 479
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL
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                                                                                                                                                                   h 47.7%; Score 329; DB 10; Similarity 100.0%; Pred. No. 4.1e-267; 29; Conservative 0; Mismatches 0;
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RESULT 5
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
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CURRENT FILING DATE: 2001-03-30
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TYPE: PRT
ORGANISM: Artificial Sequence
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; TYPE: PRT
; ORGANISM: Homo s
US-09-921-161-1
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4
LENGTH: 697
Query Match
Best Local Similarity
Matches 292; Conserv
                                                                                                                             SOFTWARE: FastSEQ
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09921161 Patent No. US20020090662A1
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/225,433
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 1
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APPLICANT: Graddis, Thomas
ITILE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                         APPLICANT: Ralph, Peter TITLE OF INVENTION: ANALYTICAL METHOD FILE REFERENCE: GENERT. 066A
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
US-09-854-356-3
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Best Local Similarity
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APPLICANT: SmithKline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/new Fusion Proteins
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EQ ID NO 3
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 4.8e-236;
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SOFTWARE:

NUMBER OF SEQ ID NOS:

PRIOR APPLICATION NUMBER: US 09/493,480 PRIOR FILING DATE: 2000-01-28 PRIOR APPLICATION NUMBER: US 60/117,976 PRIOR FILING DATE: 1999-01-29

CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09

FILE REFERENCE: 014058-009810PC

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CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKine Beecham Biologicals S.
APPLICANT: SmithKine Beecham Brologicals S.
                        APPLICANT: Cheever, Martin A. APPLICANT: Gheysen, Dirk APPLICANT: Corixa Corporation APPLICANT: SmithKline Beechar
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APPLICANT: Corixa Corporation
APPLICANT: Smithkline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
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Llarity 100.0%; Pred. No. 5.1e-236;
Conservative 0; Mismatches 0:
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FEATURE:

ORGANISM: Artificial Sequence

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CURRENT APPLICATION NUMBER: US/09/769,508
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-769-508-2
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Matches 292; Conserv
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APPLICANT: MONAHAN, JOHN J.
APPLICANT: LANGTON, BEATRRICE CLAUDIA
APPLICANT: HANCOCK, MITAM E.C.
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APPLICANT: BLUFORD, PETER

TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75

FILE REFERENCE: BEBIO-111-C1
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SEQ ID NO 1
LENGTH: 1255
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Best Local Similarity
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
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APPLICANT: Corixa Corporation
APPLICANT: Smithkline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
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LOCATION: (990)..(1255)
OTHER INFORMATION: phosphorylation domain (PD)
NAME/KEY: DOMAIN
LOCATION: (990)..(1048)
OTHER INFORMATION: fragment of the phosphorylation domain, preferred.
OTHER INFORMATION: portion (delta PD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: DOMAIN
LOCATION: (676)..(1255)
OTHER INFORMATION: intracellular domain (ICD)
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TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (1)..(653)
OTHER INFORMATION: extracellular domain (ECD)
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               NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                                                                   CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-930-125-2
                                                       US-09-441-411-6
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 Query Match
Best Local Similarity
                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
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Best Local
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APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
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NUMBER OF SEQ ID NOS:
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version
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CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/441,411
                                                                                                                                                                                                                                                                                    APPLICANT: Scholler, Nathalie B
APPLICANT: Disis, Mary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MCNeill, Patricia D.

APPLICANT: Vedvick, Thomas S.

TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hand-Zimmerman, Susan APPLICANT: Cheever, Martin A.
                                                                    LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
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100.0%; Pred. No. 8.4e-236;
tive 0; Mismatches 0;
Score :
 292; DB 9; I
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FENGTH: 1255
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Best Local S
Matches 292
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APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/602,530 PRIOR FILING DATE: 2000-06-23 NUMBER OF SEQ ID NOS: 11
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               NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                                                                CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHE 277
                                                                                                                                                ELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHPCSPM 217
                                                                 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
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100.0%; Pred. No. 8.4e-236;
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APPLICANT: Schwall, Ralph
APPLICANT: Schwall, Ralph
APPLICANT: King, Kathleen
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APPLICANT: King, Kathleen
APPLICANT: Wing, Kathleen
CURRENT SPECIES GENENT.034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT APPLICATION NUMBER: 60/189,844
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
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Search completed: April 28, 2003, 13:47:06 Job time: 24 secs
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                                                              218 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 277
                                                                                                                                                                                          CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
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Result	Score	Query Match	Query Match Length DB	DB	ID	Description
1	1587	100.0	289	22	AAE13120	Mature human HER-2
2	1587	100.0	479	22	AAE13112	Human HER300-rGM-C
w	1587	100.0	555	22	AAE13108	Human HER500 fusio
4	1587	100.0	564	22	AAE13110	Human HER500 fusio
₅	1587	100.0	645	22	AAB60408	Human ErbB2 oncopr
σ	1587	100.0	645	22	AAB61593	Human ErbB2 extrac
7	1587	100.0	653	21	AAB21200	Extracellular HER-
&	1587	100.0	653	23	AAM51145	Human Her-2/neu on
9	1587	100.0	690	22	AAE13109	Human HER500-hGM-C
10	1587	100.0	697	22	AAE13111	Human HER500-rGM-C

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AAE09208 AAE09209	AAE09207	AAE09206	AAE09205	AAE09204	AAE09203	AAE09202	AAE09200	AAE09183	AAE09181	AAE20348	AAR08222	AAR39568	AAU74545	AAU77114	AAM51143	AAE20479	AAE24067	AAB60167	AAG88267	AAB85458	AAE12130	AAY92620	AAY84780	AAB21198	AAW92406	AAW01111	AAB21208	AAY44993	AAM51148	AAB21203	AAW19764	AAM51149	AAB21204
Human Human	Human	Human	Human	Human	Human	Human	himan	n-smu+.	nemuH	Human	Extra	Seque	Humen	Human	Human	Human	Ruman	HER2	HER2/	Human	Human	Kuman	.mino	Human	Human	HER-2	Humarı	DC8sc	Her-2	3	Her2-	Her·2	Human
р68нER-2 gen р68нER-2 gen	S	N	N	ړٰ	2	N	N		р6внER-2 gen	truncated HE	Extracellular port	Sequence of c-erbB	HER2 (ErbB2)	Her-2/neu po	/neu	Her-2/neu pr		HER2 transgene pla	HER2/neu amino aci	_		heregulin 2				/neu protei		DC8scFv-erbB2EC fu	xtrac		GM-CSF immuno	extrac	HER-2/neu fu

RESULT 1 AAE13120

ALIGNMENTS

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AAE13120 standard; Protein; 289 AA. Mature human HER-2 membrane distal extracellular domain. 28-JAN-2002 AAE13120; (first entry)

Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; human; HER-2 membrane distal extracellular domain.

Homo sapiens.

WO200174855-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US10515

30-MAR-2000; 2000US-193504P

(DEND-) DENDREON CORP.

Laus R, Vidovic D, Graddis Η.

WPI; 2001-662965/76. N-PSDB; AAD21571.

An immunostimulatory fusion protein comprising the intracellular domain

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RESULT 2
AAE13112
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This sequence is used in the HER500 and HER300 GM-CSF fusion constructs
                                                                                                                                                                                               Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendrittic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CS HER-2 protein; granulocyte-macrophage colony stimulating factor; ovalbumin-derived octapeptide; OVA; rat; HER300-rGM-CSF fusion pro
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                                                                                                                                                                                                                                                                                                               Human HER300-rGM-CSF fusion construct comprising OVA-derived peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunostimulatory fusion protein comprising the intracellular domain HER-2 and an antigen elicits an immune response to the antigen and useful for the treatment of associated cancer associated - \,
                                 ocal Similarity
                                                                                                                                                                                                             granulocyte-macrophage colony stimulating factor (GM-CSF) sequence a C-terminal tag
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DB; AAD21568.
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                                                                                                                                           479 AA;
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RESULT 3
AAE13108
Immunostimulatory fusion protein: IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human;
                                                                                                                                   28-JAN-2002
                                                                                                                                                                AAE13108;
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                                                                                                     fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid molecules encoding such proteins. The IFPS comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular
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                   28-JAN-2002
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                                                                                                                                                                                 GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
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Pred. No. 1.8e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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immunostimulatory component; T-cell mediated immune residendritic cell; colon cancer; breast carcinoma; ovarian
                                                                                                Human
                                                 [mmunostimulatory
                                                                                                HER500 fusion
                                               fusion protein;
                                                                                              protein construct comprising OVA-derived octapeptide
                                                 IFP;
                                                 antigen
                                               component;
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Homo sapiens Unidentified

30-MAR-2001; 2001WO-US10515

(DEND-) DENDREON CORP

Vidovic D, Graddis H

2001-662965/76. B; AAD21566.

immunostimulatory fusion protein comprising the intracellular domain HER-2 and an antigen elicits an immune response to the antigen and useful for the treatment of associated cancer associated -

Page English.

The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 fusion protein construct which comprises human PAP signal sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodominant octapeptide, HER-2 membrane distal intracellular domain and a C-terminal tag.

564 AA; 100.0%; llarity 100.0%; Conservative Score 1587; DB 22; Pred. No. 1.9e-131; Mismatches 0; Lengt.h

STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 0, 0 Gaps 60

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STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ

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GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS

GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329

RESULT

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AAB60408

AAB60408 standard; Protein;

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AAB60408;

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                                                                                                                                                                                                                        CC The invention relates to a method for treating cancer in a human patient, CC wherein the cancer expresses epidermal growth factor receptor (EGFR), CC comprising administering an antibody which binds ErbB2 (HER2: AAB60408). CC In particular, the anti-ErbB2 antibody is the murine monoclonal antibody. CC 2c4 (AAB60396, AAB60397) or a humanised version of 2c4 (AAB60398, CC AAB60399). The invention also encompasses an isolated nucleic acid CC encoding a humanised ErbB2-binding antibody: a the recombinant production of a humanised CC comprising such nucleic acids; the recombinant production of a humanised CC erbB2-binding antibody; and an immunoconjugate comprising a humanised CC erbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies CC erbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies CC erbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies CC erbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies CC erbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies CC ext by antagonising ErbB receptors, and as inhibitors of transforming CC growth factor alpha (TGF-alpha)-activated mitogen activated protein CC especially colon cancer, rectal cancer, colorectal cancer, lung cancer, CC especially colon cancer, rectal cancer, colorectal cancer (especially colon cancer). The antibodies may also have non-therapeutic CC uses e.g., as affinity purification agents. Using an antibody which binds CC to ErbB2 as a cancer to active drug will also bind, with skin toxicity. The antibodies are anticipated to have a better safety profile than such drugs.
                                                                                                 Query Match
Best Local :
                                                                               Matches
                                                                                                                                                                                            having been observed for EGFR-targetted drugs. Antibodies ErbB2 are anticipated to have a better safety profile than The present sequence represents human ErbB2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-ErbB2 monoclonal antibody 2C4; HER2; mouse; murine; humanised; VL; light chain variable region; cancer; cytostatic; EGFR-expressing cancer; epidermal growth factor receptor; colon cancer; rectal cancer; tumour; colorectal cancer; non-small cell lung cancer; metastatic breast cancer;
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 1A; 89pp;
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Query Match Best Local Matches

Similarity

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Score 1587; DB 22; Pred. No. 2.2e-131;

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                      cell growth, differentiation and survival. The receptor family includes four distinct members including Epidermal Growth Factor Receptor (EGFR (ErbB1), HER2 (ErbB2 or p185^neu), HER3 (ErbB3) and Her4 (ErbB4 or tyro2). The present invention relates to a method for treating prostate cancer. The method comprises administering an antibody which binds ErbB2 and blocks ligand activation of an ErbB receptor. Preferably, the antibody blocks binding of monoclonal antibody 2C4 to ErbB2 and/or blocks Diggresiant activation of mitogen-activated protein kinase (MAPK). The present sequence is the extracellular domain of human ErbB2.
                                                                                                                                                                                        Treating prostate cancer in a human which binds ErbB2 and blocks ligand
                                                                                                                                                                                                                                                                               (SLOK
                                                                                                                                       The ErbB family of receptor tyrosine kinases
                                                                                                                                                                 Disclosure;
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monoclonal antibody 2C4; variable light chain.
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  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 289; Conservative 0;
                                                                                                                                                                                               The present sequence is the extracellular HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
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                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HER-2/neu extracellular domain/phosphorylation domain useful for vaccinating against breast, ovarian, colon,
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SMITHKLINE BEECHAM
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  Score 1587; DB 21;
Pred. No. 2.2e-131;
Mismatches 0;
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                                                                      The present sequence is that of the extracellular domain of human Her-2/neu (p185 glycoprotein or c-erb82), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu (see AMS1143) is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and overexpression correlates with a poor prognosis in breast and
ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or
                                                                                                                                                                                                                                                                                                                Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-)
                                                                                                                                                                                                                                                                       Claim 2;
                                                                                                                                                                                                                                                                                                      phosphorylation
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SMITHKLINE BEECHAM BIOLOGICALS.
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Best Local S
Matches 289
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                                                                                                                                                                                             Chimeric -
                                                                                                                                                                                                                                                             Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF;
  WPI;
                                                                                                             30-MAR-2001;
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                                                                                                                                                                                                                                     HER-2 protein;
HER500-hGM-CSF
                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                  30-MAR-2000;
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                                                       DENDREON CORP
                           Vidovic D,
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Synthetic.
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                                                                                                                                                                                                                                     granulocyte-macrophage fusion protein.
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                             Graddis
                                                                                                                                                                                                                                                                                                                                              protein construct.
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GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ

160

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SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS

289

220 240 280

SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS

161

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181 221 241 281

GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS

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                                                                                                                                                                                                         Matches
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                           The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 hGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature PAP protein, an Ala Arg linker, human granulocytersingual sequence, mature PAP and ala linker, a mature human granulocyter macrophage colony stimulating factor (GM-CSF) sequence and a
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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               61
                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulatory fusion protein comprising the intracellular ( {\tt HER-2} and an antigen elicits an immune response to the antigen useful for the treatment of associated cancer associated -
GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 120
                                                     STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
                                                                         STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
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                                                                                                                             Score 1587;
Pred. No. 2.4
0; Mismatches
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2.4e-131;
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RESULT 10
AAE13111

ID AAE13111 standard; Protein; 697 AA.

XX

AC AAE13111;

XX

AC AAE13111;

XX

AC AAE13111;

XX

AC AAE13111;

XX

Immunostimulatory fusion construct comprising OVA-derived peptide.

XX

Immunostimulatory component; T-cell mediated immune response; DC;

KW immunostimulatory component; T-cell mediated immune response; DC;

KW dendritic cell; colon cancer; breast carcinoma; ovarian cancer;

KW dendritic cell; colon cancer; breast carcinoma; ovarian cancer;

KW PAP protein; Ala Arg linker; membrane distal extracellular domain;

KW membrane distal intracellular domain; C-terminal tag; human; GM-CSF;

KW HER-2 protein; granulocyte-macrophage colony stimulating factor;

KW HER-2 protein; granulocyte-macrophage colony stimulating factor;

KW ovalbumin-derived octapeptide; OVA; rat; HER500-rGM-CSF fusion protein

XX

Chimeric - Homo sapiens.

OS Chimeric - Unidentified.

XX

W0200174855-A2.
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RESULT 11
AAB21204
ID AAB21
XX
AC AAB21
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AC AAB21
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AC Humar
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Best Local
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            Human HER-2/neu fusion protein
                                     12-JAN-2001
                                                               AAB21204;
                                                                                       AAB21204 standard; protein; 712 AA
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                                                                                                                                                    GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
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89; Conservative
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                                     (first entry)
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100.0%; Pr
ative 0;
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Pred. No. 2.4e-131;
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17-JUN-2002
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(first entry)
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Fig 13; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for vaccinating against breast, prostate cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HER-2/neu extracellular domain/phosphorylation domain useful for vaccinating against breast, ovarian, colon,
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breast cancer; prostate cancer; ovarian cancer; lung cancer;
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(SMIK ) SMITHKLINE BEECHAM
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standard; Protein; 712 AA
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Pred. No. 2.5e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of Her-2/neu is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltaPD intracellular domain or phosphorylation domain or phosphorylation domain (or its DeltaPD intracellular domain or phosphorylation domain or phosphorylation domain (or its DeltaPD intracellular domain or phosphorylation domain or phosphorylation domain (or its DeltaPD intracellular domain or phosphorylation domain domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Query Match
Best Local Similarity
                                                                                                                                                                       that is overexpressed in breast, ovarian can other cancer cells) and granulocyte-macrophage colony stimulating factor (GM-CSF). It is the expression product of a nucleic acid molecule (AAT72725) prepd. by PCR amplification of Her2 cDNA from a breast cancer cell line and fusion to GM-CSF cDNA. Fusion expression vectors can be used to transfect mammalian and insect cells. The Her2-GM-CSF fusion protein is used to generate anti-Her2 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo
                                                                         Sequence
                                                                                                                                                  cells are eliminated by cytotoxic T lymphocytor in vitro by exposure to antigen-presenting
                                                                                                                                                                                                                                                                                                                                                                                 A fusion protein (AAW19764) comprises Her2 (a growth factor receptor
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                                                         The present sequence is a fusion protein comprising the extracellular domain and the phosphorylation domain of the human HER-Z/neu protein. HER-Z/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-Z/neu gene is an oncogene. HER-Z/neu fusion proteins may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-Z/neu protein. They may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an extract the content protein that the prostate cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-)
                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                prostate cancers -
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SMITHKLINE BEECHAM
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Best Local S
Matches 289
          The present sequence is that of a fusion protextracellular domain and phosphorylation domaic (see AAM51143), an oncogenic self-protein and
                                                                          Her-2/neu fusion protein for treating or preventing or
or enhancing an immune response to the protein, has He
extracellular domain fused to Her-2/neu intracellular
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                                                 Claim
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                                                                                                                                                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                                                                                  tyrosine kinase;
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n protein between to domain of human plan and target for a sained by recombinations.
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response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient. Sequence vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-Z/neu protein is fused to a Her-Z/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune methods. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and 919 AA;

ş ş Ş S 밁 밁 밁 밁 Ouery Match Best Local Similarity Matches 289; Conserv 181 SRCWGESSEDCOSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS 240 202 142 LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG 121 LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG 61 GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 120 82 GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 141 22 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 1 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 60 SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS Conservative 100.0%; Score 1587; DB 23; 100.0%; Pred. No. 3.5e-131; tive 0; Mismatches 0; Indels Length 919; 0, Gaps 201 81 261 180 0

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Result
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2613.108 Million cell updates/sec
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ALIGNMENTS

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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
A; Residues: 6B:M11730; NID:g183986
R; KIng, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
Science 229, 974-976, 1985 A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 R:Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985 A;Title: A v-erbB-related protooncogene, c-erbB-2, 1s distinct from the c-erbB-1/epid A;Reference number: A23491; MUID:86016729; PMID:2995967 A;Accession: A25491 RESULT 1 A24571 A;Reference number: 137622; MUID:87286898; PMID:3039351
A;Recession: 157622
A;Stacus: translated from GB/EMBL/DDBJ
A;Molecule trne-nw* C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C;Accession: A24571; A25491; A44188; B44188; I59509; I57622 A;Molecule type: DNA
A;Residues: 740-910 <COU1>
A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989
A;Accession: B44188 R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to A;Reference number: A44188; MUID:86070181; PMID:2999974
A;Accession: A44188 A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growt A;Reference number: A24571; MUID:86118663; PMID:3003577 A;Accession: A24571 A; Molecule type: DNA A: Residues: 1-191 <TAL> A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808 R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, Mol. Cell. Biol. 7, 2597-2601, 1987 A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma. A;Reference number: I59509; MUID:85272597; PMID:2992089
A;Accession: I59509 A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein A; Molecule type: DNA A; Residues: 832-909 <REX> A;Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 737-1031 <SEM> A; Molecule type: mRNA A; Residues: 1-1255 <YAM> R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, Nature 319, 230-234, 1986 K.; Nomura, N.; Miyajima, N.; Saito, PID: 9553282 A.; McGrath, EGF receptor shares chro Givol, o J.; Seeburg

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A;Title: The new oncogene encodes an epidermal growth factor receptor-rel A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Recession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R;Masul. T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat new oncogene transmembrane doma 2-thiazolyl]formam.de or N-methyl-N-nitrosourea.
                                                                                                                                                                                                                                                                          protein-tyrosine kinase (EC 2.7.1.112) neu precursor C;Speckes: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #t C;Accession: A24562; A61204 R;Bargmann, C:I; Hung, M:C.; Weinberg, R.A. Nature 319, 226-230, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:676-1255/Domain: Intracellular #status predicted <INT>
F:718-983/Domain: protein kinase homology <KIN>
F:718-983/Domain: protein kinase homology <KIN>
F:726-734/Region: protein kinase ATP-binding motif
F:686,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status F:686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:753/Active site: Lys #status predicted
F:7139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphoryl
    A;Reference number: A61204; MUID:92035293;
A;Accession: A61204
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
C;Function: catalyzes the phosphorylation of a peptidyl tyrosine residue
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprote
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A;Cross-references: GDB:120613; OM
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Matches 289
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rons: 25/1; 75/3; 147/1; 883/3
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Pred. No. 2.6e-109;
; Mismatches 0;
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C;Superfamily: epic
C;Keywords: ATP
F;718-983/Domain: F
F;726-734/Region: F
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les 247; Conserv
YVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQL 121
                                             TQVCTGTDMKLRLPASPETHLDIVRHLYQGCQVVQGNLELTYLPANATLSFLQDIQEVQG
                                                                                                                                                  Similarity
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F;731-739/Renion nutry autophosphorylation; duplication; glycoprotein; phosphores; 1-19/Domain: signal sequence #status predicted <SIG>F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>F;68-680/Domain: transmembrane #status predicted <TMN>F;731-739/Renion protein kinase homology
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F;731-739/Region: protein kinase ATP-binding motif
F;731,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent)
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                    Gene 140, 251-255, 1994
A;Title: Cloning and activation
A;Reference number: I48161; MUII
A;Accession: I48161
                                                                                                                                                                                                                                                                                                                                                                                                                                                       p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golder
C;Date: 02-7u1-1996 #sequence_revision
C;Accession: I48161
                                                                                                                                                                                                                                                                                        A; MOLECULE type: mRNA
A; Residues: 1-1254 < RES>
                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA; Molecule type: DNA; Residues: 637-663,'V',665-702; Note: authors translated the
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TQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQG
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                                                                                                                                                                                                       epidermal
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki,
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                     GB:D16295; NID:g493236; PIDN:BAA03801.1;
                                                                                                                                                                                                         growth factor receptor;
                                                                               83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.3%;
85.5%;
                                                                                                                                                                                                                                                                                                                                                                          cion of the Syrian hamster neu
MUID:94193007; PMID:7908275
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                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (golden hamster)
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                                                                                                                                             ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1353.5; DB 1;
Pred. No. 4.4e-92;
Pred. No. 4.4e-92;
                                                                               Score 1322;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                 from GB/EMBL/DDBJ
                                                              Mismatches
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                                                                                                    Length
                                                              Indels
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                                                                                                                                                                                                         kinase homology
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epidermal growth factor receptor precursor - chicken N;Contains: protein-tyrosine kinase (EC 2.7.1.112) e. C;Species: Gallus gallus (chicken) C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #. C;Accession: A27720; A00643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Molecule type: mRNA
A:Residues: 1-327 <FLI>
A:Cross-references: GB:M77637; NID:g211737; PIDN:AAA48759.1; PID:g211738
A:Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MR; Filckinger, T.W.; Maihle, N.J.; Kung, H.J. Mol. Cell. Biol. 12, 883-893, 1992
A; Title: An alternatively processed mRNA from the avian A; Reference number: A42032; MUID:92123214; PMID:1732751 A; Accession: A42032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermal growth factor receptor - C; Species: Gallus gallus (chicken)
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C;Accession: A42032
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mes 139; Conserv
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                                                                                                                                                                                                                                    GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 289
                                                                                                                                                                                                                                                                                                                                             RLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PLTVLDFASNLSSCPKCHPNCTED
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                                                                                                                                                                                                                                                                                                 RCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor receptor
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48.1%; Pred. No. 3.9e-47;
tive 48; Mismatches 90
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                                                                                       05-May-1995 #text_change
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A; Residues: 585-1223
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Cell 41, 719-726,
                                                                                                                         rg, P.H.
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Best Local
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F;719-984/Domain: protein kinase homology <KIN>
F;727-735/Region: protein kinase ATP-binding motif
F;727-735/Region: protein kinase ATP-binding site: carbohydrate (Thr) (covalent)
F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;169/Binding site: carbohydrate (Thr) (covalent) (by protein kinase C) #status predicte
F;754/Active site: Lys #status predicted
F;754/Active site: Lys #status predicted
F;7100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;31-1223/Product: epidermal growth factor receptor #status
F;31-654/Domain: extracellular #status predicted <EXT>
F;81-307/Domain: EGF receptor extracellular domain repeat <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;678-1223/Domain: intracellular #status predicted <INT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:M10066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M20386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: epidermal growth factor receptor; protein kinase homology; Superfamily: epidermal growth factor receptor; protein; glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-1223/Product: epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                         63 VLIAHNOVROVPLORLRIVRGTOLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 KVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLEITYVEHNRDLTFLKTIQEVAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGY 62 :|| || :|| || :|| :|| :|| :|| :|| :||
                                                                                                        SLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID-TNRSRACHPCSPMCKGS
GICELHCPALYTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                                                                                                                                                                                                                         RLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PLTVLDFASNLSSCPKCHPNCTED
                                                                                                                                                                                                                                                                                                                                     VLIALNMVDVIPLENLQIIRGNVLYDNSFALAVLSNYH-MNKTQ-----;--GLRELPMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in ALV-induced erythroblastosis: MUID:85228222; PMID:2988784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodwin, R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 739; DB 1; Length 1223; 
Pred. No. 9e-47; 
8; Mismatches 90; Indels J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rottman, F.M.;
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313
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RESULT 6
GOHUE

epidermal growth factor receptor precursor - human
N;Conttains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999.
C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143;
C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143;
C;Accession: A00641; A25, 1984
A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression
A;Reference number: A00641; MUID:84219729; PMID:6328312
A;Accession: A00641
A;Residues: 1-1210 <UILL>
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
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Pastan,

Binding

of,

EGF

6

the receptor leads

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internalization

of

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EGF-recepto

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A;Accession: A05281
A;Molecule type: protein
A;Residues: 25-30 'S',32-51;454-467 <WEB>
A;Residues: 25-30 'S',32-51;454-467 <WEB>
A;Residues: 25-30 'S',32-51;454-467 <WEB>
T. Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros
J. Biol. Chem. 260, 5205-5208, 1985
A;Title: Identification of residues in the nu-
A;Reference number: A60143; MUID:85182650; PM
A;Reference number: A60143; MUID:85182650; PM
A;Recession: A60143
A;Molecule type: protein
A;Residues: 740-744 'X',746-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Natura 300, 270-273
                                                         Nature 309, 270-273, 1984
A;Title: ATP-stimulated interaction between epidermal growth A;Title: exp-stimulated interaction between epidermal growth A;Reference number: A38023; MUID:84191554; PMID:6325948
A;Contents: annotation; receptor activity
A;Note: the EGF receptor (and other tyrosine kinases) can nic R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C. Cell 59, 33-43, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-32
', 798-799, 'TD', 802-811, 'R', 813-942 <XUY>
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF rece
R; Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I
Science 224, 843-848, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A00642; MUID:84245835; PMID:6330563 A;Accession: A00642 A;Molecule + 1000
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J. Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription & A;Reference number: A38672; MUID:91107677; PMID:1988448
A;Accession: A38672;
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A; Residues: 1028-1210 <SIM>
R: Weber, W.; Gill, G.N.; Spa
Science 224, 294-297, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: epidermoid carcinoma cell | R; Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, Biochem. Biophys. Res. Commun. 124, 125-132, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: carcinoma cel R; Xu, Y.; Ishii, S.; Clark, A.J.L.; Nature 309, 806-810, 1984
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A;Title: The human EGF receptor gene: structure of the A;Reference number: S30024; MUID:88217333; PMID:3329716
A; Title: Functional independence of the epidermal growth factor A; Reference number: A33331; MUID:90003233; PMID:2790960
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A; Residues: 1-29 <HAL>
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A; Residues: 1-29 <HA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A05281; MUID: 84172183; PMID: 6324343
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[Xu, Y], Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma; D.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:M11234; NID:9181981; PIDN:AAA52370.1; PID:9553272; Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield,
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4.L.; Schulz, T.Z.; Wright, D.A.; Ca
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S.; Staros,
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24, 1985
                                                                                                                                                                                                                                                                                                                                                                                 nucleotide binding PMID: 2985580
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PMID:2991899
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epidermal growth factor receptor precursor - mouse ;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999 C;Accession: A53183; A43818; S24942; A28941; S45325; I49643 R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jei Genes Dev. 8, 399-413, 1994 A;Ritle: The mouse waved-2 phenotype results from a point mutation in the E(A;Reference number: A53183; MUID:94170986; PMID:8125255
submitted to the EMBL Data
A; Reference number: S24942
A; Accession: S24942
A; Molecule type: mRNA
                                                                                                                                        A; Reference number: A431
A; Accession: A43818
A; Molecule type: mRNA
A; Residues: 1-714 <AVI>
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F;25-645/Domain: extracellular #status predicted <EXT>
F;75-300/Domain: EGF receptor extracellular domain repeat <EE1>
F;390-600/Domain: EGF receptor extracellular domain repeat <EE2:
F;646-668/Domain: transmembrane #status predicted <TMM>
                                                                                          A;Cross-references: GB:X59698 R;Eisinger, D.P.; Serrero, G.
                                                                                                                                                                                                                                     A; Title: Comparison of
                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:U03425
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A; Residues: 1-1210 <LUE>
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F:710-975/Domain: protein kinase homology <KIN>
F:718-726/Region: protein kinase ATP-binding motif
F:7999-1046/Region: coated-pit mediated internalization s
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C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphol
E; 1-24/Domain: signal sequence #status predicted <SIG
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                                                                                                                                                                                                                                                         A.; Lax, I.; Ull
6, 673-676, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCKDTCPPLMLYNPTTYQMDVNPEGKYSEGATCVKKCPRNYVVTDHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
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                                                                                                                                                                                                             of EGF receptor sequences A43818; MUID:91232866; PMI
                                                                                                                                                                                                                                                                                    Ullrich,
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                                                                    Library,
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Pred. No. 4.1e-45;
4; Mismatches 99;
                                                                                                                                                                                                                                                                                 Schlessinger,
                                                                                                                                                                                                               Ces as a guide
PMID:2030916
                                                                                                                                                                                                                                                                                 J.; Givol,
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F;648-670/Domain: transmembrane #status predicted <rmm>
F;712-977/Domain: protein kinase homology <KIN>
F;712-977/Domain: protein kinase ATP-binding motif
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
F;107/Binding site: phosphate (Tyr) (covalent) #status experimental
  epidermal growth factor receptor, HER4 - human C;Species: Homo sapiens (man) C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999 C;Accession: A47253 R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009
A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009
A;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A;Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor
                                                                                                                      RESULT
A47253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA, A;Residues: 1-971, Kr, 973-1210 <VER>
A;Residues: 1-971, Kr, 973-1210 <VER>
A;Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA55587.1;
R;Parla, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A;Title: Expression of the epidermal growth factor receptor ger A;Reference number: I49643; MUID:93126380; PMID:7678348
A;Accession: I49643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 12-20,22-132 <RES>
A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
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A; Cross-references:
R; Helsermann, G.J.;
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Accession: A47,
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Best Local
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                                                                                                                                                                                                              QDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGS
                                                                                                                                                                                                                                                      NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                                                                                                                                                                                                                                                                                                   PNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAGCTGPRESDCLVCQKF
                                                                                                                                                                                                                                                                                                                                                                                             NLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL----QSHPSSCPKCDPSC
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                                                                                                                                                                                                                                                                                                                                                  KGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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3.J.; G111, G.N.
263, 13152-13158, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.1%; Score 716.5;
47.3%; Pred. No. 4.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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  Carlton, G.W.;
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A; Molecule type: nucleic acid
A; Residues: 1-1308 <PLO>
A; Residues: 1-1308 <PLO>
A; Cross-references: GB:LO7868; NID:g337359; PIDN:AAB59446.1;
A; Note: sequence extracted from NCBI backbone (NCBIP:126842)
C; Superfamily: epidermal growth factor receptor; protein kine
C; Keywords: ATP; growth factor receptor
F; 716-981, Domain: protein kinase homology <KIN>
F; 724-732/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Ligand-specific activation of HER4/p180er
A:Reference number: A47253; MUID:93189574; PMID:83
A:Accession: A47253
                                                                                                                                                                                                                                                        A;Ressioues: 1704 A;Ressioues: GB:M37394 A;Cross-references: GB:M37394 C;Superfamily; epidermal growth factor receptor; protein kinase C;Superfamily: alternative splicing; ATP; growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: A36325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Rattus norvegicus (Norway ra
C; Date: 25-Jan-1991 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 10, 2973-2982, 1990 A; Title: A truncated, secreted form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Petch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A36325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L.A.; Harris,
                                                                                                                                                        QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSF1.QDIQEVQGY
                                                                            VLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR 122
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SLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRS-RACHPCSPMCKGS
                                                                                                                     KVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGY
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                                                                                                                                                                                                   Pred. No. 8.5
l; Mismatches
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Pred. No. 4.4e-45
7; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.C.;
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181
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NLQEILIGAVRFSNNPILCNMETIQWRDIV-QDVFLSNMSMDVQRHLTGCPKCDPSCPNG

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epidermal growth factor receptor homolog precursor N;Alternate names: ErbB3 protein; HER3 protein C;Species: Rattus norvegicus (Norway rat) C;Date: 17-Jan-1996 #gennoncommon rat)
                                                          RESULT 11
JC4387
epidermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;ATRAUS, M.H.; ISSING, W.; MIKI, T.; Popescu, N.C.; ABATONSON, S.A. Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A;Title: Isolation and characterization of ERBB3, a third member of A;Reference number: A36223; MUID:90083234; PMID:2687875
A;Accession: A36223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000 C;Accession: A36223; I59164
R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
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A;Gross-references: GDB:119880; OMIM:190151
A;Map position: 12q13-12q13
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
A;Title: Mclecular cloning and expression of another epidermal growth factor A;Reference number: 159164; MUID:90311312; PMID:2164210
A;Accession: 159164
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A36223
kinase-related transforming protein (erbB3) (EC
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A;Residues: 1-559,'G',561-957,'F',959-1063,'G',1065-1342 <RES>
A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; P
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A; Residues: 1-1342 <K
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Cross-references: GB:M29366
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2/Domain: protein kinase homology <KIN>
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                                                                                                                                                               SGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFV 295
                                                                                                                                                                                                     SGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYL 283
                                                                                                                                                                                                                                                                             SRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNH
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Pred. No. 8e-43;
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  #text_change 13-Nov-1998
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A; Residues: 821-102.
A; Cross-references: C; Genetics:
        A; Nedwar type: DNA
A; Residues: 821-1025, 'N', 1027-1098, 'A', 1100-1166 <ADA>
A; Residues: 821-1025, 'N', 1027-1098, 'A', 1100-1166 <ADA>
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                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1166 <WIT>
                                                                                                                                                                                                                                                                                                    Nature 341, 415-421, 1989
A; Title: Novel putative re
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                                                                                                                                                                                                                                                             A; Accession: S06142
                                                                                                                                                                                                                                                                             A; Reference number: S06142;
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A;Molecule type: mRNA
A;Residues: 1-1339 (HELDA)
A;Cross-ferences: GHELDA
A;Cross-references: GHELDA
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R; Hellyer, N.J.; Kim, H.H.; Greaves, C.H.;
Gene 165, 279-284, 1995
A; Title: Cloning of the rat ErbB3 cDNA and
A; Reference number: JC4387; MUID:96096535;
A; Accession: JC4387
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F:705-970/Domain: protein kinase homology <KIN>
F:713-721/Region: protein kinase homology of the protein fill the protein kinase homology of the protein fill the prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 FTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRVR---GAEIVVKNNGANCPPCHEVCKG
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SGACVPRCPEPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFV
                                                                                                                                      SGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTGPKHEDCLACLHFNH
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                                                                                                                                                                                                                                                                                                                                                                                        -RCWGPGPDDCQILTKTICAPQCNGRCFGPNPNQCCHDECAGGCSGPQD?; DCFACRRFND
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Pred. No. 2.6e-40;
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A;Reference number: S13807; MUID:91125882; PMID:1846957
A;Accession: S13809 A;Cross-references: EMBL:X16891; NID:g65290; R;Adam, D.; Maeueler, W.; Schartl, M. Oncogene 6, 73-80, 1991 C;Date: 10-Sep-1999 #sequence_revision C;Accession: S06142; S13809 R;Wittbrodt, J.; Adam, D.; Malitschek, protein-tyrosine kinase (EC 2.7.1.112) mrk-y precursor - southern platyfish N;Alternate names: epidermal growth factor receptor homolog; kinase-related C;Species: Xiphophorus maculatus (southern platyfish) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000 A; Status: preliminary; translation D.; Malitschek, B.; Maeueler, W.; receptor eptor tyrosine kinase encoded MUID:90015140; PMID:2797166 not shown PIDN:CAA34770.1; bу Raulf, the Xmrk oncogene PID: g65291 melanoma-inducing F.; Telling, 'n transform Xiphoph Robe Tu

PIDN:CAA39763.1;

PID: 965285

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A;Gene: mrk
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A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C;Superfamily: epidermal growth factor receptor; phosphotransferase; transmembrar F;1-25/Domain: signal sequence #status predicted <SIG>F;26-1166/Product: kinase-related transforming protein (Tu) #status predif;707-972/Domain: protein kinase homology <KIN>F;715-723/Region: protein kinase ATP-binding motif
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Cell 46, 1091-1101, 1986
A;Title: Alternative 5' exons and tissue-specific expression
A;Title: Alternative 5' exons and tissue-specific expression
A;Title: Alternative 5' exons and tissue-specific expression
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                                                                                                                                                                                                                                                                                                                                                                                                                   ;Cross-references: FlyBase:FBgn0003731
;Superfamily: epidermal growth factor receptor; protein kinase homology
;Keywords: ATP; growth factor receptor
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                                                                                                                                                                                                                                                                         QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT-NASLSFLQDIQEVQG 61
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SCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDCIAC
                                       MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 234
                                                                                 YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE
                                                                                                                        RELQUESCITETLKGGVLTQRNPQLCYQDTTLWKDIFHKNNQLALTLIDTNRSRACHPCSP 176
                                                                                                                                                                    YILISHVDVKKVVFPKLQIIRGRTLFSLSVEEEKYALFV-----
                                                                                                                                                                                                       YVLIAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASPGGL 116
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Pred. No. 1.6e-39;
                                                                                                                                                                                                                                                                                                                                                        Score 536; DB 2;
Pred. No. 5.9e-32;
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                                                      protein-tyrosine kinase (EC 2.7.1.112) let-23 precursor NyAlternate names: receptor tyrosine kinase let-23 C;Species: Caenorhabditis elegans C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text C;Accession: S70712; S73101; S13422; T27682
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C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases;
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A;Title: Genome sequence of the nematode C. elegans: a platform A;Reference number: A75000; MUID:99069613; PMID:9851916
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C;Species: Caenorhabditis elegans
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R;Sakai, T.; Koga, M.; Ohshima, Y
J. Mol. Biol. 256, 548-555, 1996
A;Title: Genomic structure and 5'
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A; Residues: 1-1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Caenornauurus cury...;Date: 10-May-2001 #sequence_revision;Date: E88257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          see websites genome.wustl.edu/gsc/C_elegans/ apublished_errata appeared in Science 283, 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN----
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                                                                                                                                                                                                                                                                        GASCVTACP 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89; Conser
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A;Reference number: S70712; MUID:96177760; PMID:8604137 A;Accession: S70712

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A; Residues: A; Molecule type: A;Status:

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R;Arolan, R.V.; Koga, M.; Mendel
Nature 348, 693-699, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 28.8%; Proceedings of Conservative 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Map position: 2
introns: 44/1; 51/1; 90/1; 112/3; 165/3; 217/1; 290/1; 379/1; 418/1; 448/2; 565/1; 60
superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol.
Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein k
1-28/Domain: signal sequence #status predicted <SIG>
29-1374/Product: protein-tyrosine kinase let-23 #status predicted <MAT>
934-1199/Domain: protein kinase homology <KIN>
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Molecule type: DNA
Residues: 52-1374 <WIL>
Cross-references: EMBL:270038; PIDN:CAA93882.1; GSPDB:GN00020; CESP:ZK1067.1
EXPERIMENTAL SOURCE: Clone ZK1067
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Accession: T27682
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Residues: 52-1374 <ARO>
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Residues: 1-50,'G',52-1374 <KOG>
Cross-references: EMBL:D63426; NID:g1407562; PIDN:BAA09729.1; PID:g1407563
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                                                                                                              370 GNHCVKECP 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VHEVVMRELRVIRNGSVTIODNPKMCYIGDKIDWKELLYDPD--VQ 250
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Pred. No. 1.9e-21;
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      SwissProt_40:*
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      DB
SFPO_HUMAN
ERBB_ALV
PRP1_HUMAN
ODO2_MYCTU
EXTN_TOBAC
EGFR_MOUSE
SM6B_MOUSE
PRP2_HUMAN
IRS2_MOUSE
TEGU_EBV
MAPA_HUMAN
ICPO_HSV11
WAIT_HUMAN
ICPO_HSV11
WAIT_HUMAN
TPM4_DROME
DNAA_STRCO
EBN4_EBV
APG_BRANA
PRP3_MOUSE
EXLP_TOBAC
VGLG_HSV2H
CC01_CAEEL
YMO91_NPVOP
XP2_XENLA
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EGFR_HUMAN
ERB4_HUMAN
ERB4_RAT
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P233246
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P042
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homo sapien
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homo sapien
homo s
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4 rattus norv
4 mus musculu
3 homo sapien
5 rattus norv
6 homo sapien
6 rattus norv
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1 mycobacteri
nicotiana t
saccharomyc
l orgyia pseu
7 xenopus lae
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USE	IAL). ULAR LO	e phosp			N	zation o	94196; Low J.,	L-654 A	Acad.	idermal ary qla	elated	16729;	37.	:1132-1	inase r	Seebur Levins			230-234	rowth f	oyoshim of pro	, Ikawa	OM N.A.	9606;	Metazoa utheria	R2 OR N	eptor H	otein-t	(Rel.	(Rel.	STA						90			
USE			"Ē	EGULINS ND FOR	99. 199.	of a new	Wallace	ND VAL-	Sci. U.	growth nd aden	protoon	PubMed=	FRO	139(198)	eceptor	: =		PubMed=	(1986).	actor re	a K.; tein en	S., Ak	Dishwod.		; Chorda ; Prima:	GL OR NI	roto-one ER2) (MI	yrosine	05, Lasi	05, Crea	NDARD;			040	ם בי	44	o 7	φ μ	04	•
USE	e H	TH EA	+	DO NOT IN	PONENT	allele izatio	95488; R.B.,		S.A. 82:64	factor-re	cogene, c.	2995967;	Z	. \$: 5	Libermanr Jllrich A	L., Liao	2999974 :					٠,			žU.	ogene) (C	kinase er	sequence	ted)	PRT;		ALTO							
P52734 mus P78706 neu P05142 mus P05142 mus P05142 mus P061473 mus P061473 mus P10162 home P10162 home P10162 home P10162 home P10162 home P10162 home P101610 home P10162 home P101	embrane protein.	OF THE OTHER ERBB	n tyrosine •	ACT WITH IT	F A NEUREGULIN-	f the human ERBB2	A.M.;		497-6501(1985).	gene and i	, is distinc	; =		en olicogene.	homology to	T.A., Schlessing	C., Chen E., Gra				c-erb-B-	K., Nomura N			Vertebrata; 1 ; ноminidae;		-erbB-2) (Tyros	bB-2 precursor	e update)		1255		SUNENTS							
mus muscull neurospora mus muscull rattus nor, homo sapier mus muscull mus muscull mus muscull mus muscull romi; jima N., o o OMPLEX, OIS A , TGF- , TGF- tein		ECE .	P + pro	NE. GP3	EPTOR C					anplit	from					_ ر	٠.>					•			uteleos Homo.		inase	7.1	. ·					055196 Q64355	043281	09y4h2 006852	09wv46	Q61473	P52734	1 1
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-!- SUBCELLULAR LOCATION: Type I membrane protein.

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Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain.
Pfam; PF02757; YLD.
              TRANSMEM
DOMAIN
DOMAIN
DOMAIN
BIND
BINDING
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DISULFID
                                                                                                                                                                                                                                                                       SMART; SM00261; FU; 3.
SMART; SM00219; TYFK; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene f;
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InterPro;
InterPro;
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Genew;
MIM; 1
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           W; HGNC:3430;
164870; -.
                                                                                                                                                                                                                                                                                                                                                                                   ); IPR000494; EGFR_L_domain.
); IPR000719; Euk_pkinase.
); IPR000174; Futin-1ike.
); IPR001245; Tyr_pkinase.
); IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a license agreement (S
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                 Tyrosine-protein
     ERBB2
                                                                                                                                                                                                                                                                                                                                                                                                                      EGFR_L_domain.
Euk_pkinase.
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JOINED.
JOINED.
JOINED.
JOINED.
POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PROTEIN KINASE
PROTEIN KINASE
ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                       POTENTIAL.
RECEPTOR PROTE
                                                                                                                                                                                                                                                                 kinase;
                                                                                                                                                                                                                       PROTEIN-TYROSINE LULAR (POTENTIAL)
                                                                                                                                                                                                                                                               e family; Reco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                                                                                              Receptor; Signal;
ing; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                 KINASE ERBB-2
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Best Local Similarity
Matches 216; Conserv
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Q60553;
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CARBOHYD
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DISULFID
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DISULFID
                                                                                                                      TISSUE-Nerve;
MEDLINE-94193007; PubMed-7908275;
Nakamura T., Ushijima T., Ishizaka
Yamazaki Y., Ishikawa T.;
"Cloning and activation of the Syri
Gene 140:251-255(1994).
                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUNN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor
(p185erbB2) (NEU proto-oncogene) (C-erbB-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _MESAU
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                                      -
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                    Mesocricetus auratus (Golden hamster)
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                       ERBB2 OR NEU.
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FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LICAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RES
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187
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629
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AA; 137909
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Rodentia;
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99.5%;
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Pred. No. 3
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P -> A (IN REF. 2).
W; 39E9DFDA04DCF962 CRC64;
                                                                                                                                                                                                                                                                                                      Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId-VAR_004077.
                                                                                                                                                                                                                                                                                                                      Craniata;
                                                                                                                                            Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                              hamster
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thi; Muridae; Cricetinae;
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                                                                                                                                            proto-oncogene.";
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(POTENTIAL).
SUBCELLULAR LOCATION
PTM: LIGAND-BINDING

LOCATION: Type I membrane protein.
-BINDING INCREASES PHOSPHORYLATION

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TYROSINE

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Interpro; iPR002174; Furin like.
Interpro; iPR001245; Tyr_pkinase.
Interpro; iPR001245; Tyr_pkinase.
Interpro; iPR004019; YLP_motif.
Pfam; pF00069; pkinase; 1.
Pfam; pF00757; Furin-like; 1.
Pfam; pF00757; Furin-like; 1.
Pfam; pF00757; YLP; 2.
Pfam; pF02757; YLP; 2.
Pfam; pF02757; YLP; 2.
Pfam; pF002751; FLP; 3.
SMART; SM00201; FU; 3.
SMART; SM002019; TYFKC; 1.
PROSITE; PS00109; PROTEIN_KINASE_ATPROSITE; PS00109; PROTEIN_KINASE_ATPROSITE; PS00109; PROTEIN_KINASE_ATPROSITE; PS00109; PROTEIN_KINASE_TYPROSITE; PS00109; PROTEIN_KINASE_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TYPROSITER_TY
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InterPro; IPR000719; Euk_pkinase.
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PS00109; PROTEIN_KINASE_TYR; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
ibrane; Glycoprotein; Multigene family; Receptor; Signal; brane; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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Receptor protein-tyrosine kinase erbb-2 precursor (EC 2.7.1.112)
(p185erbb2) (NEU proto-oncogene) (C-erbb-2) (Epidermal growth far receptor-related protein).
ERBB2 OR NEU.
Rattine page 14.
                                                                        oncogenic and oncogenic forms of the new protein.";

EMBO J. 11:43-48(1992),

-I- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EG
ALPHA AND AMPHIREGULIN.

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + pr
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MEDLINS-92155181; PubMed-1346763;
MINE-1181-92155181; PubMed-1346763;
MEDLINS-92155181; PubMed-1346763;
MEDLINS-9215181; PubMed-1346763;
MEDLINS-9215181; PubMed-1346763;
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MEDLINE-91222560;
Lai C., Lemke G.;
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MEDLINE-86118662; PubMed-3945311;
Bargmann C.I., Hung M.-C., Weinberg R.A.;
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                                                                                                                                                                                                                                                                                                                                              "An extended family of protein-tyrosine kinase genes expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutherla; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The neu oncogene encodes an epidermal growth protein.";
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membrane protein ONCOGENIC VARIANT

ERBB RECEPTORS

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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene family;
Transmembrane; Glycoprotein; Multigene family;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A24562; TVRTNU.
P11362; TFGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION RESIDUES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00757;
PF01030;
PF02757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000494;
IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001245; Tyr_pkinase. IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Furin-like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pkinase;
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654
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Euk_pkinase.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY)
BY SIMILARITY
BY 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family; Receptor; kinase; ATP-binding; Phosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nere are no rest
as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                 (AUTO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eptor; Signal;
Phosphorylation;
                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                    (POTENTIAL).
                                                                                                      (BY SIMILARITY).
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CD-1; TISSUE-Uterus;
STRAIN-CD-1; TISSUE-Uterus;
MEDLINE-97200814; PubMed-9048643;
Lim J., Dey S.K., Das S.K.;
"Differential expression of the e
                                                                                                                                                                                                                                                                                                                                                        "Synapse-associated expression of an acetylcholine receptor-inducing protein, ARIA/heregulin, and its putative receptors, ErbB2 and ErbB3, in developing mammalian muscle.";
Dev. Biol. 172:158-169(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 150-245 FROM N.A. MEDLINE=96069911; PubMed=7589796; Moscoso L.M., Chu G.C., Gautam M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P70424; Q61525;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation.update)
15-JUN-2002 (Rel. 41, Last annotation.update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse uterus: potential mediator o factor-like growth factors."; Endocrinology 138:1328-1337(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1220
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sanes J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NEU proto-oncogene) (C-erbB-2) ERBB2 OR NEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
                                                                                                                                                                                                              tyrosine SUBUNIT:
                                                                                                     SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: E)
CELLS. IN THE MUSCLE,
OF MUSCLE FIBERS.
DEVELOPMENTAL STAGE: ON DAYS 1-4 OF PREGNANCY, ERBB2 1: PRIMARILY IN EPITHELIAL CELLS, THE DAY 1 UTERUS SHOWING HIGHEST ACCUMULATION. ON DAY 5, THE EPITHELIUM AND THE DECIDUALIZING STROWAL CELLS AROUND THE IMPLANTING BLASSE EXHIBIT ACCUMULATION OF THIS RECEPTOR. ON DAYS 6-8, THE
                                                                                                                                                                                                                                              FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR CON ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, ALPHA AND AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protections of the protein tyrosine = ADP + Protections of tyrosine = ADP + Protections of tyrosine = ADP + Protections of tyrosine = ADP + ADP +
                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _MOUSE
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Rodentia;
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81.6%;
                                                                                                                        N: Type I membrane protein.
EXPRESSED PREDOMINANTLY IN UTERINE EPITHELIALE, EXPRESSION LOCALIZES TO THE SYNAPTIC SITES
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Sciurognathi;
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thi; Muridae;
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                                                                                                                                                                                                              OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.G., Merlie
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                                                            ERBB2 IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.P.,
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3P30 IS A
3GF, TGF-
                                                                DETECTED
THE
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InterPro; IPR004040; STY_pkinase.

InterPro; IPR004040; STY_pkinase.

InterPro; IPR001245; Tyr_pkinase.

R PRINTS; PR00109; TYRKINASE.

R ProDom; PD000001; EUK_pkinase; 1.

R SMART; SM00221; STYKC; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.

R PROSITE; PS001109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

Transmembrane; Glycoprotein; Multigene family; Receptor; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                               EGFR_HUMAN STANDARD; PRT; 1210 AA. P00533; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG 000688; Q9BZS2; Q9H2C9; Q9GZX1; Q9H3C9; 21-JUL-1986 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epidermal growth factor receptor precursor (Epideria) 15-JUN-2010e kinase ErbB-1).
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MEDLINE-84219729; PubMed-6328312;
UllTich A., Coussens L., Hayfilck J.S., Dull T.J., Gray A., Tam A.I

Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,

Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;

"Human epidermal growth factor receptor cDNA sequence and aberrant
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                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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Biochem.
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Lin C. R., Chen W.S., Kruiger W., Stolarsky L.S., Weber W.,
Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
"Expression cloning of human EGF receptor complementary. DNA:
amplification and three related messenger RNA products in A4:
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                                                                                                        O'Malley B.W.;
                                                                                                                                Simmen F.A.,
                                                                                                                                               MEDLINE-85046483;
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85046483; PubMed=6093780;
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.J.;
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L., Threadgill D.W., Danielsen A.J.,
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        OF 1-29
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Strunk K.E., Danielsen P.J., Yee D., Lampland son T.R., James C.D.,

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                    A431 epidermoid
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identification of sequences regulating its
Oncogene Res. 1:375-396(1987).
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and supercoiled DNA.";
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Haley J.D., Whittle
Waterfield M.D.;
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56:881-914(1987).
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MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex. Induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family, as TGF-alpha, amphiregulin, betacellulin, heparin-bindi EGF-like growth factor, Gp30 and vaccinia virus growth factor. involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alternative splicing.
TISSUE SPECIFICITY: Expressed
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ALTERNATIVE PRODUCTS:
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SUBCELLULAR LOCATION:
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-PERGAPPSTFKGTPTAENPEYL
|: | ||: ||| |||
FPKEAKPNGIFKGS-TAENAEYL
                                                               VFAFGGAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----
                                                                                                                                                          SEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET-
                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produ
                                                                                             DDTFL-----PVPEYINQ-SVPKRPAGSVQNPVYHNQPLNP-----
                                                                                                           SSPSTSRTPLLSSLSATSN--NSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSI 1082
                                                                                                                                                                                                                                       U48725;
U48726;
                                                                                                                                                                                                                                                                                    X00588;
U95089;
U48722;
                                                                                                                                                                                                                                                               U48724;
                                                                                                                                                                                         62; Conserv
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                                                                                                                                                                                                                                                                                                                                                requires a license agreement
                                                                                                                                                                                                                                                                                                                                   email to license@isb-sib.ch).
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                          this statement is not removed.
                                                                                                                                                                                                                                     CAA25240.1;
AAB53063.1;
AAC50802.1;
AAC50804.1;
AAC50796.1;
AAC50797.1;
AAC50798.1;
                                                                                                                                                                                                    13.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type I membrane protein. Isoform 2 is
                                                                                                                                                                                         24;
                                                                                                                                                                                        Score 164; DB
Pred. No. 0.00
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isoforms;
                       212
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                                              PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDF
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uced by
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RRR OCC GDE DTT
                                                                                                                                                                              RESULT 6
ERB4_HUMAN
                                                                                           15-DEC-1998 (Rel. 37, Created)
.15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor
(pl80erbB4) (Tyrosine kinase-type cell surface rec
SEQUENCE FROM
TISSUE-Breast
                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                      ERB4_HUMAN Q15303;
                                                                      Homo sapiens
                                                                                  ERBB4 OR HER4.
                                  NCBI_TaxID=9606
                                                                      (Human)
 N.A. (ISO
                                                                                                                                                                  STANDARD;
           (ISOFORM JM-A)
                                              Chordata;
Primates;
                                              Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                  1308
                                                                                                                                                                  ş
                                                Hominidae;
                                                                                             receptor
                                                                                                        (EC
                                                            Euteleostom1;
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Plowman G

MEDLINE-93189574; PubMed-8383326;

Neubauer M.G., Shoyab M.

.D., Culouscou J.-M., Whitney G.S., Green J.M.,

Carlton G.W.,

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PRODOM; PDUUUUL, 4.

SMART; SM00219; FU; 4.

SMART; SM00219; TYTKC; 1.

SMART; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Ligand-specific activation of HER4/p180erbB4, a fourth member of the epidermal growth factor receptor family."; Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                    CHAIN
DOMAIN
                                                                                                                                                                                                                                     Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
Pfam; PF02757; YLP; 2.
                                                                                                                                                                                                                                                                                                             InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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Klagsbrun M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Fetal brain;
MEDLINE-97476287; P
   TRANSMEM
                                                        Alternative splicing SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 600543;
                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L07868; AAB59446.1; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phorbol ester."
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS JM-A AND JM-B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; JAM A (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER
FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED
BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND
NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN
CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,
KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROLD, CEREBELLUM,
PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS,
LUNG, SALLVARY GLAND, AND PANCREAS.
LUNG, SALLVARY GLAND, AND PANCREAS.
LUNG, SALLVARY GLAND, AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 272:26761-26768(1997).

FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTORS (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC: 3432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific stribution and differential processing in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corfas G.,
26
26
652
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1308
651
675
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                                                                                                                                                                                                                                                                                                                                                                                                                        ERBB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paul S., Choi C.J., Rio C., Plowman G.D
                  POTENTIAL.
RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on
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### AIN ### 496 ### 633 ### CYS-RICH. ### 496 ### 683 ### CYS-RICH. ### CYS-RICH. ### SIMILARIT ### SI	111340	DЪ	Qy	Дb	Qy	pb .	QV	Db	Qy	Db	Qy	Query Best Match	SQ		HJ H			Ε •						FT T			E T			FT			H T		F 7				-		H	-	3 1
CYS-RICH. CYS-RICH. CYS-RICH. CYS-RICH. CYS-RICH. CYS-RICH. BY SIMILARITY. BY SIMILARIT	7	270		210 NT	176	176	27 GATLE	127	4	067		Match Local S es 62	EQUENC	VARSPLIC	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	MOD_RES	MOD_RES	MOD_RES	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	DISULFID	ACT_SITE	BINDING BINDING	DOMAIN	DOMAIN	DOMAIN
CYS-RICH. CYS-RICH. CYS-RICH. CYS-RICH. CYS-RICH. CYS-RICH. BY SIMILARITY. BY SIMILARIT		RPIVAENE	AENE	FLGKAEYI	,			PTVFAPER	ເວ	AAEQGVSV	OLTLGLE-	larít Conse	308	626	5/6 620	548	495	410	358	181	174	1284	1258	1162	621	593	580	5 5 5 5 5 5 5	536	507	503	308	293	249	234	217	213	189	843	724 751	718	496	0/6
CYS-RICH. CYS-RICH. CYS-RICH. PROTEIN KINASE ATP (BY SIMILARITY). ATP (BY SIMILARITY). BY SIMILARITY. BY SIMILA		128	N	KNNILSMPEK		KNGDLQ	3KNGVVKDVFA	RSPRGELDEEG	:	PYRAPTSTIP	PSEEEAPRSP	13.3%; 24.2%; ative 2	146807	648	5/6 620	548	495	410	358	181	174	1284	1258	1162	633	614	589	569	552	520	512	323	304	258	246	229	221	197	843	732 751	985	633	o c
10 10 00				DYWNHSLPPRSTLQHPDYLGEYSTKYFYK 12	SPAFDNLYYWDQDPPERGAPPSTFKGTPT 20	ALDNPEYHNASNGPPKAEDEYVNEPLYL 12	GGAVENPEYLTPQGGAAPQPHPPPA 17	YMTPMRDKPKQEYLNPVEENPFVSRR 1	A 12	11	7	Score 157; DB 1; Length 1308; Pred. No. 0.012; 3; Mismatches 75; Indels 96; Gap	N ISOFORM JM-B). 5E4AE80985D88761 CRC64;	PTSHDCIYYPWTGHSTLPQHA -> IGSSIEDC	LINKED (GLCNAC)	LINKED (GLCNAC) (POTENTIAL)	LINKED (GLCNAC) (POTENTIAL)	LINKED (GLCNAC) (POTENTIAL)	LINKED (GLCNAC) (FOTENTIAL)	LINKED (GLCNAC) (LINKED (GLCNAC) (POTENTIAL	OSPHORYLATION (AUTO-) (BY SIMILARITY)	PHORYLATION (AUTO-) (BY SIMILARITY)	PHORYLATION (AUTO-) (BY SIMILARITY)	SIMILARITY.									SIMILARIT	SIMILARIT	SIMILARITY	SIMILARITY	ດທ	SIMILARITY.	(BY SIMILARITY)	SE.	CYS-RICH.	

RESULT 7

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THE PROPERTY OF A PROPERTY OF 
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MEDLINE-97184212; PubMed-9030624;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.
"Expression of neuregulins and their putative re
ErbB3, is induced during Wallerian degeneration.
                                                                                                                                                                                         EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ErbB3, is induced during Wallerian degeneration.";

J. Neurosci. 17:1642-1659(1997).

-I- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
-I- RUNGTON: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.

NOT ACTIVATED BY EGF., TGF-A, AND AMPHIREGULIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel Marchionni M.A., Kelly R.A.; "Neuregulins promote survival and growth or Persistence of ErbB2 and ErbB4 expression ventricular myocytes.", J. Biol. Chem. 273:10261-10269(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   062956; Q9Z2N7;
15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor
ERBB4 OR TYRO-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERB4_RAT
Q62956; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine phosphate.
-1- SUBUNIT: HOMODIMER OR HETERODIMER WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOT ACTIVATED BY EGF, TGF-I- CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "An extended family of prote expressed in the vertebrate Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Sciatic ne
MEDLINE-91222560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                       or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1031-1198 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 848-901 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTORS (POTENTIAL).

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELO
NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIL
                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Electropean Bioinformatics Institute. There are no restricted to the state of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C., Lemke G.
                                                                                                                                                                                         AF041838;
U52531; AA
P11362; 1F
                                                                                                                                                                                                                                                                                                                s requires a license agreement (
an email to license@isb-sib.ch)
                                                           IPR000494; I
IPR000719; I
IPR002174; I
IPR001245; T
                                                                                                                                                                                         AAC53051.1;
1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                           AAD08899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9553078;
r D.R., Baliga R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2025425
                                                                                                                       EGFR_L_domain.
Euk_pkinase.
                                                           Tyr_pkinase
                                                                                                Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-tyrosine kinase
                                                                                                                                                                                                                                              1; -.
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Sciurognathi; Muridae;
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tors, ErbB2
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PROSITE: PSO0101; PROTEIN_KINASE_DOM; 1.
PROSITE: PSO0109; PROTEIN_KINASE_TYR; 1.
PROSITE: PSO0109; PROTEIN_KINASE_TYR; 1.
Transmembrane; dlycoprotein; Multigene family; Rece
Transferase; Tyrosine-protein kinase; ATP-binding;
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Pfam;
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PF01030;
PF02757;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Splicing factor, proline-and glutamine-rich (Polypyrimidine tract-binding protein-associated splicing factor) (PTB-associated splicing factor) (PSF) (DNA-binding P52/P100 complex, 100 kDa subunit).
SPPQ OR PSF.
Homo sapiens (Human).
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Biochem. J. 290:267-272(1993).

SPLICEDSOME FORMATION. BINDS TO THE MAMMALIAN POLYPYRIMIDINE SPLICEDSOME FORMATION. BINDS TO THE POLYPYRIMIDINE TRACT-BINDING TRACTS. FORMS A COMPLEX WITH THE POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB). SEEMS TO ALSO BIND DNA.

1- SUBCULIVE HETEROTETRAMER OF TWO 52 KDA AND TWO 100 KDA SUBUNITS.

1- SUBCELLULAR LOCATION: Nuclear.

1- SUBCELLULAR LOCATION: Nuclear.

1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM: (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).

1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE MYOBLAST CELL SURFACE ANTIGEN 24.1D5 AND A POSSIBLE MEMBRANE-BOUND PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90091812: PubMed=2480877: Gower H.J., Moore S.E., Dickson G., Elsom V.L., Moore S.E., Moore S.
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   EMBL; X70944; CAA50283.1;
EMBL; X16850; CAA34747.1;
PIR; A43557; A43557.
PIR; S29770; S29770.
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93176127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 48-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal brain;
MEDLINE=93194059; PubMed=8449401;
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                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEKAKKAFDNPDYWNHSLPPRSTLQHPDYLQEYSTKYFYKQNGRIRPIVAENPEYL
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PSF,
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                                                                                                                                                                                                                                                                             There are no restrictions ng as its content is in
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                                                                                                                                                                                                              http://www.isb-sib.ch/announce/
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l pre-mRNA
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l surface a
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Homo.
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RESULT 9
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Best Local S
Matches 58
                                                                                                     21-JUL-1986
15-JUL-1999
15-JUN-2002
       SEQUENCE FROM N.A.
MEDLINE-8522822; PubMed-2988784;
Nilsen T.W., Maroney P.A., Goodwin R.G.,
Crittenden L.B., Raines M.A., Kung H.-J.;
"c-erbB activation in ALV-induced erythro
                                                                                                                                ERBB_ALV P00534;
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000504; RNA_rec_mot.
pfam; pF00076; rrm; 2.
SMART; SM00360; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                   Avian leukosis virus.
Viruses; Retroid viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternative
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                                                          NCBI_TaxID=11864;
                                                                                      V-ERBB.
                                                                                             Tyrosine-protein kinase
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                                                                                                                                                                                     PTPPPAVTSA------PP--GAPPPTPPSSGVPT
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                                                                                                                                                                                                                      KPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGA----
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58; Conserv
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297 36
371 45
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707
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(Rel.
(Rel.
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promoter
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                                                                                                                                        STANDARD;
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38,
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insertion
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                                                                   Retroviridae;
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                                                                                                                                                                                                                                                                                                                           Score 145.5; DB Pred. No. 0.033; L3; Mismatches E
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POLY-GLN.
POLY-PRO.
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RNA-BINDING (RRM)
3 X 3 AA REPEATS
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RTERFGQGGAGPVGGQGPRGMGPGTPAGYGRGREEYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; mRNA splicing; Repeat;
         erythroblastosis:
result in expression
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on update)
g protein
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                                                                   Alpharetrovirus
                         Rottman
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                                                                                                                                                                                                                                                                                         -SPPPGMGLNQNRGPMGPGPGQS 54
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novel
ion of
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RESULT 10
PRP1_HUMAN
ID PRP1_
AC P0428
DT 20-MA
DT 13-AU
DT 16-OC
DE Saliv
GN PRB1.
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Best Local S
Matches 54
----CTT-2001 (Rel. 05, La
----CCT-2001 (Rel. 40, Las
Salivary proline-rich prol
[Contains: Basic pept' a
PRB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0109; TYRKINASE.

ProDom; PD000001; Euk_Pkinase; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00109; PROTEIN_KINASE_ATP;

PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a center the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                    P04280;
                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase InterPro; IPR001245; Tyr_pkinase pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M10066; AAA48763.1; ALT_INIT. PIR; A00643; TVCHLV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino-truncated EGF :
Cell 41:719-726(1985
                                                                                                                     PRP1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM;
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MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP +
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                                                                                                                                                                                      QINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP
                                                                                                                                                                                                                                                                                                                                                                                  RSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--
                                                                                                                                                                                                                   ----DPPE----
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                                                                                                                                                                                                                                                                                                                                                         RTPLLSSLSATSNNSATNCID-----RNGQGHPVREDSFVQRYSSDPTGNFLEESID
                                                                                                                                                                                                                                               SLTAISKLPMDSRYQNSHSTAVDNPEYL
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                                                                                                                                                                                                                                                                                                     DGFL-----PAPEYVNQ--LMPKKPS-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
138
165
257
634
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                                                                                                                     STANDARD;
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                               . 40, Last annotation update) rich protein precursor (Clones peptide IB-6; Peptide P-H].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 1
257 1
70891 MW;
                                                                                                                                                                                                                  RGAPPSTFKGTPTAENPEYLGLDVP
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24.5%;
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                                                           Last sequence up
                                                                                         Created)
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ATP (BY SIMILARITY).
BY SIMILARITY.
; E705E33A0BE01FCC CRC64;
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No. 0
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                                               CP3,
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                      Repeat;
SIGNAL
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SEQUENCE FROM N.A.
MEDLINE-85289325; PubMed-2993301;
MEDLINE-85289325; Azen E.A., Smithles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kauffman D., Hofmann T., Bennick A., Keller P.; "Basic proline-rich proteins from human parotid covalent structures of proteins IB-1 and IB-6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maeda N., Kim H.-S., Azen E.A., Smithles O.;
"Differential RNA splicing and post-translational human salivary proline-rich protein gene system.", J. Biol. Chem. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                        PIR; A03291; PIHUB6.
PIR; C25372; C25372.
Genew; HGNC:9337; PRB1.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; K03204; AAA60185.1; -. EMBL; K03205; AAA60186.1; -. EMBL; K03206; AAA60187.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84161824; PubMed-6671974;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry
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Mammalia; Eutheria;
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                                                                                                                                                                    RSSSTRSGGGDLTLGLEPSEEEAPRSPLAP---SEG---AGSDVFDGDLGMGAAKGLQSL
                        PHPPPAFSPAFDNLYYWDQDPPERG-----
                                                                                                                      PTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPS-----PR--- 116
                                                                                                                                            KSRSPRSPPGK-PQGPPPQGGNQPQGPPPPPGKPQGPPPQGGNKPQGPPPPGKPQG----
                                                                                               ----PPPQGDKSQSPRSP-PGKPQG-----
                                               NRPOGPPPPGKPOGPPPOGDKSRSPOSPPGK-
                                                                                                                                                                                             64;
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                                                                     -EGPLPAARPAGATLERAKTLS----PGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              saliva and complete
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                                                                                                                                                                                                                                     276
331
                                                                                                                                                                                            Conservative
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276
106
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32596
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331
238
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Primates;
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25.5%;
-QGPPPQGGNKPQGPPPPGKPQGPPAQGGSKSQSARAPPGKPQ
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                                                                                                                                                                                          Score 135.5;
Pred. No. 0.06
L7; Mismatches
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PEPTIDE P-H.
MISSING (IN CLONE (
FTIG-VAR_005561.
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/FTId-VAR_005562.
A -> S (IN REF. 2 AND 3)
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                                                                                                                                                                                                                                          3F481FF8EBA39751
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sequence of basic proline-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
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GTPTAE - - NPE

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OC Bacter

OC Bacter

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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Ha:
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holro
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Elsen J.A., Gwinn M.L., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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15-JUN-2002 (Rel. 41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Tricarboxylic acid cycle.
SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
SYMMETRY (BY SIMILARITY).
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PATHWAY: Tri
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P07016; 1C
MT2272; -.
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AAK46557.1;
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Matches 56
                                                                                                                                MEDLINE-90128263; PubMed-2612909,
MEDLINE-90128263; PubMed-2612909,
Keller B., Lamb C.J.;
Keller B., Lamb C.J.;
Keller B., Lamb C.J.;
Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene in lateral root initiation.";
Genes Dev. 3:1639-1646(1989).
-1- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERHIS OF
                                                                                                                                                                                                                                                                                                        Nicotlana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotlana. NCBI_TaxID-4097;
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ACT_SITE
SEQUENCE
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InterPro; IPR003016; Lipoyl.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00364; biotin_lipoyl; 2.
Pfam; PF02817; e3_binding; 1.
ProDom; PD001115; 20xoacid_dh; 1
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMUL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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01-JAN-1990 (Rel. 13,
16-OCT-2001 (Rel. 40,
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                                                                                                 SUBCELLULAR LOCATION: Extracellular matrix.

PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN
                                                                                       GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPAPEPPPVQPTSGAPAGGDAKPVLMPELGESVTEGTVIRWLKKIGDSVQVDEPLVEVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSLPTHDPSPLQ-----RYSEDPTVPLPSETD--GYVAPLTCSPQPEYVNQPDVRPQP-
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162 L
523 B
527 B
57087 MW;

    Last sequence update)
    Last annotation update)
    (Cell wall hydroxyproline-rich glycoprotein)

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BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 0.11;
4; Mismatches
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or send a
                    STRAIN-BALB/c, and CD-1; TISSUE-Liver, and Decidua; MEDLINE-93126380; PubMed-7678348; Paria B.C., Das S.K., Andrews G.K., Dey S.K.; "Expression of the epidermal growth factor receptor in mouse blastocysts during delayed implantation."; Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                           Avivi A., Skorecki K., Yayon A., Givol D., "Promoter region of the murine fibroblast (bek/KGFR) gene."; Oncogene 7:1957-1962(1992).
                                                                                                                                                                                                                                                                             STRAIN-BALB/c; TISSUE-Liver; MEDLINE-93026370; PubMed-1408137;
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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Q01279;
                                                                                                                                                   SEQUENCE FROM N.A.
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15-JUN-2002
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Cell wall;
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an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
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EXTENSIN.
H-A-P-P.
H-A-P-P.
2 X 7 AA T.
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3 X APPROXIMATE TAN
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                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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    EMBL; X78987; CAAS5587.1; -
EMBL; U03425; AAA17899.1; -
EMBL; X59698; CAA42219.1; -
EMBL; L06864; AAA53029.1; -
EMBL; Z12608; CAA78249.1; -
HSSP; P11362; 1FGK.
MGD; MGI:95294; Egfr.
                                                                                                                                                                                                                                                                                Pfam; PF00069; Pfam; PF00757; Pfam; PF01030;
TRANSMEM
DOMAIN
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MEDLINE-91232866; PubMed-2030916; 
                                            CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed: entities requires a license agreement (See or send an email to license@isb-sib.ch).
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[5]
                                                                                  Tyrosine-protein SIGNAL 1
                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                               SMART; SM00261; FU; 3.
SMART; SM00219; TYTKC; 1.
                                                                                                                                                                                                                                                           Pfam; PF01030; Recep_L_domain; ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
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Genes Dev. 8:399-413(1994).
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Luetteke N.C., Phillips H.K., Qiu
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BALB/C; TIS H1bbs M.L.;
                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The mouse waved-2 phenotype recentor tyrosine kinase.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SUBCELLAUGAR LOCATION: Type I membrane protein.
MISCELLAUGAR LOCATION: Type I membrane protein.
MISCELLAUGUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of
synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitted (JUN-1992) to the EMBL/GenBank/DDBJ databases. FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SI AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                              IPR000494; IPR000719; IPR002174; IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6:673-676(1991).
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                                                                                                                                                                                                                                                                                                      pkinase; 1.
Furin-like; 1.
                                                                                                                                 Glycoprotein;
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                                                                                                           kinase;
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                                                                                                                                                                                                                                                                                                                                                                      Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                               EGFR_L_domain.
                                                                                                        ein; Receptor; Signal; Transfe;
ATP-binding; Phosphorylation;
                                   POTENTÏAL.
EPIDERMAL GROWTH FACTOR R
EXTRACELLULAR (POTENTIAL)
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                                                                                               MSLDNPDYQQDFFPKETKPNGIFKG-PTAENAEYLRVAPP 1203
                                                                                                                                                                                                                    TLSPGKNGVVKDVFAFGGAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----
                                                                                                                                                                                                                                                                                                                                                                              DVVDADEYLIPQQGFFNSPSTSRTPLLSSLSATSNNSTVACINRNGSCRVKEDAFLQRYS
                                                                                                                                                                                       --APGRDLHYQN--PHSNAVGNPEYLNTAQ-----
                                                                                                                                                                                                                                                                                    SDPTGAVTEDNIDDAFL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 26.4
58; Conservative
                                                                                                                                           -DP---
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                                                                                                                                 PERGAPPSTFKGTPTAENPEYLGLDVP
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                                                                                                                                                                                                                                                                               -----PVPEYVNQ-SVPKRPAGSVQNPVYHNQPLHP-----
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BY SIMILARITY.

BY SIMIL
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APPROXIMATE.
SER-RICH.
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                                                                                                                                                                                         - PTCLSSGFNSPALWIQKGSHQ
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                                                                                                                                           217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76;
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MEDLINE-98027184; PubMed-9361278;
MEDLINE-98027184 F., Behar O., Calautti E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: DURING DEVELOPMENT IT IS EXPRESSED
-!- TISSUE SPECIFICITY: DURING DEVELOPMENT IT IS EXPRESSED
SUBREGIONS OF THE NERVOUS SYSTEM AND IS PARTICULARLY PR
MUSCLE. IN ADULTHOOD, IT IS EXPRESSED UBIQUITOUSLY.
-!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel transmembrane semaphorin can bind c-sr
Mol. Cell. Neurosci. 9:409-419(1997).
-!- SUBUNIT: HOMODIMER. BINDS SPECIFICALLY THE
PROTOONCOGENE C-SRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM6B_MOUSE
054951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01403; Sema; SMART; SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF036585; AAC00493.1; -. MGD; MGI:1202889; Sema6b.
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                                          729
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                                                                                                                         GAGG-----RSPLAPS 41
                                                                EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL-PSETDGYVAPLTC----
                                       HALGSRAWDHSHALLSASASTSLLLLAPA---RASEQPQVPAEPGPESRLCAPRSCRASH 785
                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
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----SPOPEYVNOPDVRPQPPSPREG-PLPAARPAGATLERAKTLSPGKNG---
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(Rel.
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Rel. 40, Last annotation update)
precursor (Semaphorin VIB) (Sem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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Sema.
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                                                                                                                                                                                                                                                                                                   ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEMAPHORIN 6B.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
SEMA.
POLY-LEU.
                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC...
N-E5F56D125CDA574D C
                                                                                                                                                                                                             Score 130.5;
Pred. No. 0.33
%3; Mismatches
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REPEAT
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"Complete amino acid sequence of a from human parotid saliva.";
J. Biochem. 93:883-888(1983).
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MEDLINE-85289325; PubMed-2993301;

Maeda N., Kim H.-S., Azen E.A., Smithles O.;

Maeda N., Smithles O.;

Maeda N
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Homo sapiens (Human).
Homo ryota; Metazoa; Chordata; Metazoa; Primates;
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13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sallvary proline-rich protein precursor (Clone CP7) [Contains: Basic pepide P-F] (Fragment).
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Search completed: April 28, 2003, 13:40:16 Job time: 8.53595 secs

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EGFR_MOUSE
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HTK7_HYDAT
INSR_DROME
IRE_CAVPO
MIPR_LYMST
IRE_MOUSE
IRE_MOUSE
IRE_HUMAN
INSR_RAT
IGIR_HUMAN
IGIR_HUMAN
IGIR_HOMAN
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INSR_BAEDAE
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8 xiphophorus
2 drosophila
8 caenorhabdi
6 branchiosto
7 hydra atten
8 drosophila
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1 mus musculu
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SEQUENCE FROM N MEDLINE-8607018 COUSSENS L., Yai MCGTATH J., Seel FTRANCKE U., Lev "Tyrosine kinase shares chromoson Science 230:113: 3 SEQUENCE OF 737 MEDLINE-8601672: Semba K., Kamatt "A v-erbB-relate c-erbB-1/epider human salivary proc. Natl. Acad proc. Natl. Acad [4] VARIANTS VAL-65. MEDLINE-9319419 Ehsani A., Low "Characterizati Genomics 15:426 -1- FUNCTION: E: Genomics 15:426 -1- FUNCTION: E: Genomics 15:426 -1- FUNCTION: E: GENOMICS 15:426 -1- GUBUNLT: HE: GENOMICS 15:426	B2_HUMAN ERB2_HUMAN ERB2_HUMAN P04626; 13-AUG-1987 (Rel. 05, C 13-AUG-1987 (Rel. 05, L 15-JUN-2002 (Rel. 41, L Receptor protein-tyrosi (p185erbB2) (NEU proto- surface receptor HER2) ERBB2 OR HER2 OR NGL OF ERBB2 OR HER2 OR NGL OF ERBB2 OR HER2 OF ENBB2 OR HER2 OF ENBB2 OR HER2 OR NGL OF OR HER2 OR NGL OF ENBB2 OR HER2 OR NGL OF ENBB2 OR HER2 OR NGL OF SEQUENCE FROM N.A. MEDLINE-86118663; PubMe Yamamoto T., Ikawa S., Saito T., Toyoshima K.; Ssito T., Toyoshima K.;	105.5 105 104 103.5 101.5 100.5 100 98 97 96.5 96.5
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EMBL; M11730; AAA35808.1; J

EMBL; M11730; AAA35808.1; J

EMBL; M12036; AAA35978.1; -

EMBL; X03363; CAA27060.1; -

EMBL; A24571; A24571.

PIR; A24571; A24571.

HSSP; P11362; IFGK.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
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PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
"ransmembrane; Glycoprotein; Multigene family; Receptor; Signal;
"ransmembrane; Glycoprotein kinase; ATP-binding; Phosphorylation;
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POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FRED OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.2 ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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PF02757;
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SM00261; FU;
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MEDLINE-86118662; PubMed-3945311;
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Nature 319:226-230(1986)
[2]
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Mammalia; Eutheria;
NCBI_TaxID=10116;
  SEQUENCE OF 85:
TISSUE-Sciatic
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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ERB2_RAT STANDARD; PRT; 1257 AA.

P06494;

01-JAN-1988 (Rel. 06, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)

(p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth fact receptor-related protein).

ERBB2 OR NEU.
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expressed in the vertebrate n

Neuron 6:691-704(1991).

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STRUCTURE BY NMR OF 650-668.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X03362; CAA27059.1; ALT_INIT PIR; A24562; TVRTNU. HSSP; P11362; 1FGK.
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      | L | SEQUENCE ... SEQUENCE ... TISSUE=Nerve; TISSUE=Nerve; Pub... Pub... 1: "~kamura T., Ushijima T., 1: Tshikawa T.; Tsh
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Yamazaki '
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Gene 140:
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G00553;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor
(p185erbB2) (NEU proto-oncogene) (C-erbB-2).
ERBB2 OR NEU.
                                                                                                                                                              NCBI_TaxID=10036;
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Mammalia; Eutheria;
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247; Conserv
    a T., Ushijima T.
i Y., Ishikawa T.
g and activation (
0:251-255(1994).
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ima T., Ishizaka
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Chordata; Craniat
Rodentia; Sciurog
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Pred. No. 5.7e-107;
Pred. No. 5.7e-107;
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Sciurognathi; Muridae;
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Euteleostomi; Cricetinae;

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InterPro: IPR004019; YLP_motif.
Pfam; Pr00069; pkinase; 1.
Pfam; Pr00757; Furin-like; 1.
Pfam; Pr01030; Recep_L_domain; 2.
Pfam; PF02757; YLP; 2.
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or send a
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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SMART; SM00219; TyrKc; 1
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- SUBUNIT: HETERODIMER WITH EACH OF THE CATALYTIC ACTIVITY OF THE CACH OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE
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SUBCELLULAR LOCATION:
PTM: LIGAND-BINDING I
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an email to license@isb-sib.ch).
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BY SIMILARITY BY SI
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Best Local Sin
Matches 240;
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01-JAN-1990 (Rel.
01-JAN-1990 (Rel.
15-JUN-2002 (Rel.
Epidermal growth)
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Calliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
SEQUENCE
             -
                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-88261272; PubMed-3260329;
                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                (Fragment)
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                           tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane prote
MISCELLANEOUS: Binding of EGF to the recept
dimerization, internalization of the EGF-re
induction of the tyrosine kinase activity,
synthesis, and cell proliferation.
                  synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                          CHICK
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Pfam; PF01030; Recep_L_domain; 2.
SMART; SM00261; FU; 4.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-11ke.
InterPro; IPR001245; Tyr_pkinase.
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 SLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID-TNRSRACHPCSPMCKGS
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                          VLIALNMVDVIPLENLQIIRGNVLYDNSFALAVLSNYH-MNKTQ-----
                                                VLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR 122
                                                                         KVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLEITYVEHNRDLTFLKTIQEVAGY
                                                                                                                             139;
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PS50011;
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09; PROTEIN_KINASE_TYR; 1
11; PROTEIN_KINASE_DOM; 1
Glycoprotein; Receptor;
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                                                                                                                                                                           46.6%;
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Pred. No. 3.6e
48; Mismatches
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POTENTIAL:
CYTOPLASMIC (PO
BY SIMILARITY.
BY SIMIL
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MEDLINE-84219729; PubMed-6328312;

Ullrich A., Coussens L., Hayfilck J.S., Dull T.J., Gray A., Tam A.W.
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;

"Human epidermal growth factor receptor cDNA sequence and aberrant
expression of the amplified gene in A431 epidermoid carcinoma cells
Nature 309:418-425(1984).
isoforms.
Genomics
[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95382957; pubMed-7654368; Ilekis J.V., Stark B.C., Scoccia B.; Ilekis J.V., Stark B.C., Scoccia B.; Possible role of variant RNA transcripts in epidermal growth factor receptor expression Mol. Reprod. Dev. 41:149-156(1995).
                                                                                                                                                                                                  MEDLINE-21100872; PubMed-11161793;
Reiter J.L., Threadgill D.W., Eley
Schehl Sinclair C., Pearsall R.S.,
Balasubramaniam S., Crossley T.D.,
                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gynecol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Reiter J.L., Maihle N.J.;
"A 1.8 kb alternative transcript from the human epidermal growth factor receptor gene encodes a truncated form of the receptor.";
Nucleic Acids Res. 24:4050-4056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                         Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ilekis J.V., Gariti J., Niederberger 
"Expression of a truncated epidermal 
protein (TEGFR) in ovarian cancer."; 
Gynecol. Oncol. 65:36-41(1997).
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Green P.J., Yee D.,
Magnuson T.R., Jame
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SEQUENCE Reiter J. Lampland

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575-687 FROM N.A. , Threadgill D.W., Danielsen A.J., L., Balasubramaniam S., Crossley T

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amplification and three related messenger
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*ATP-stimulated 
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J. Biol. Chem. 264:10667-10671(1989).
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                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for continuous content is not removed.
                                                                                                                                                                                                                                                expressed in ovarian cancers.
MISCELLANEOUS: Binding of EGF to the receptor lead dimerization, internalization of the EGF-receptor induction of the tyrosine kinase activity, stimula synthesis, and cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                        family, as TGF-alpha, amphiregulin, betacellulin, heparin-bindi
EGF-like growth factor, GP30 and vaccinia virus growth factor.
involved in the control of cell growth and differentiation.
FUNCTION: Isoform 2/truncated isoform may act as an antagonist.
CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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truncated isoform/TEGFR,
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SUBCELLULAR LOCATION:
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MEDLINE-93026370; PubMed-1408137;
AVIVI A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast growth (bek/KGFR) gene.";
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Q01279;
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Aviv1 A., Lax FROF receptor sequences as a
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MEDLINE-94170986; PubMed-815255;
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Epidermal growth factor
                                    "Comparison of
binding site.";
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                      6:673-676(1991)
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Metazoa; Chordata; C
™ heria; Rodentia; !
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       EMBL; X78987; CAA55587.1; -. EMBL; U03425; AAA17899.1; -. EMBL; X59698; CAA42219.1; -. EMBL; L106864, AAA53029.1; -. EMBL; Z12608; CAA78249.1; -. HSSP; P11362; 1FGK.
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SMART; SM00261; FU; 3.
SMART; SM00219; TYFKC; 1.
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Pfam; PF00757; Furin-like;
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CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP +
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complinduction of the tyrosine kinase activity, stimulation.
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IPR000719; Euk_pkinase.
IPR002174; Furin-like.
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TISSUE-Breast carcinoma;
MEDLINE-93189574; PubMed-8383326;
Plowman G.D., Culouscou J.-M., Wh
Foy L., Neubauer M.G., Shoyab M.;
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[15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.
[p180erbB4] (Tyrosine kinase-type cell surface receptor
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Mammalia; Eutheria;
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Pred. No. 5.
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Catarrhini;
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
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J. Biol. Chem.
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                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER
FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED
BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND
NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH IS EXPRESSED IN THE HEART.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,
KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROLD, CEREBELLUM,
PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS,
LUNG, SALLVARY GLAND, AND PANCREAS.
LUNG, SALLVARY GLAND, AND PANCREAS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUKEGULINS, NRG-2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELULIN AND NTAK. INTERACTION WITH THESE FACTORS INDICES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
SUBUNIT: HOMODIMER
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                              http://www.isb-sib.ch/announce/
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modified and this statement is not removed. Usage by and for comme entities requires a license agreement (See http://www.isb-sib.ch/annc or send an email to licenseeisb-sib.ch).

EMBL; L07868; AAB59446.1; -.

EMBL; L07868; AAB59446.1; -.

EMBL; L07868; AAB59446.1; -.

Genew, HGNC:343; ERBB4.

MIM; 600543;
InterPro; IPR000494; EGFR_L_domain.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR0007174; Furin-like.

InterPro; IPR0002174; Furin-like.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR01245; Tyr_pkinase.

InterPro; IPR01245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

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RESULT 8
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                                                                            SGACVTQCPQTEVYNPTTFQLEHNFNAKYTYGAFCVKKCPHNEV
                                                                                                   SGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYL
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Similarity 48.6%;
38; Conservative
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  InterPro; IPRO0-
Pfam; PF00757; I
Pfam; PF00069; I
Pfam; PF01030; I
Pfam; PF02757; V
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10116;
                                                               InterPro;
InterPro;
                                                                                                   EMBL; U52531; HSSP; P11362; InterPro; IPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley: TISSUE-Spinal cord; MEDLINE-97184212; Pubmed-9030624; Carroll S.L., Miller M.L., Frohnert P.W., "Expression of neuregulins and their putaterba; is induced during Wallerian degener J. Neurosci. 17:1642-1659(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Neuregulins promote survival and growth c
Persistence of ErbB2 and ErbB4 expression
ventricular myocytes";
J. Biol. Chem. 273:10261-10269(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor
ERBB4 OR TYRO-2.
Rattus norvegicus (Rat)
                                                                                                                EMBL; AF041838; AAD08899.1; -. EMBL; U52531; AAC53051.1; -. HSSP; P11362; 1FGK.
                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE-91222560; Pub
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Marchionni M.A., Kelly R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98221155;
                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, HEPARIN BINDING EGF-LIKE GROWTH FACTOR, BETACELULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY). CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                  PTM:
                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVZLOPING NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                                                                                                                                                                                                         European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                        RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF
                                                                                                                                                                                                                                                                                                                                                                            RECEPTORS (POTENTIAL). SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH
                                                                                                                                                                                                                                                                                                               HEART
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                                                p; IPR000494; EGFR_L_domain.
p; IPR000719; Euk_pkinase.
p; IPR0027174; Furin-like.
p; IPR001245; Tyr_pkinase.
p; IPR004019; YIP_motif.
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brate nervous system.";
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Transmembrane; Glycoprotein; Multigene family; Rece
Transferase; Tyrosine-protein kinase; ATP-binding;
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Phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                             Katoh M., Yazaki Y., Sugimura T., Terada M.;
"C-erbB3 gene encodes secreted as well as transmemb
tyrosine kinase.";
Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-I- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS
-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLING-90083234; PubMed-2687875;

Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.

"Isolation and characterization of ERBB3, a third member ERBB/epidermal growth factor receptor family: evidence fo overexpression in a subset of human mammary tumors.";

Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plowman G.D., Whitney G.S., Neubau
Todaro G.J., Shoyab M.;
"Molecular cloning and expression
factor receptor-related gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence up. 15-JUN-2002 (Rel. 41, Last annotation)
                                                                                                                                                                                                                                                                                    MEDLINE-93282822; PubMed-7685162;
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90311312; PubMed-2164210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERBB3 OR HER3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor protein-tyrosine kinase (c-erbB3) (Tyrosine kinase-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P21860;
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                                                                                              SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.

DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESID
AND PROMOTES ITS ASSOCIATION WITH THE BB5 SUBUNIT OF
PHOSPHATIDYLINOSITOL 3-KINASE (BY SIMILARITY).

DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: SECRETED (SHORT FORM)
                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: TWO FORMS,
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G.S., Neubauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             t annotation update)
kinase erbB-3 precursor
e-type cell surface recep
                                                                                                                                                                                                                                                         TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           87:4905-4909(1990)
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Pfam; PF00069; pkinase; 1.

Pfam; PF000757; Furin-like; 1.

Pfam; PF01030; Recep_L_domain; 2.

Pfam; PF01030; Recep_L_domain; 2.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TyrKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; FA
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
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InterPro; IPR000719; Euk_pkinase
InterPro; IPR002174; Futin-1ike.
InterPro; IPR001245; Tyr_pkinase
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Genew; HGNC:3431;
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L; M34309; AAA35979.1
L; S61953; AAB26935.1
; A36223; A36223.
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PROTEIN KINASE.
ATP (BY SIMILARITY
BY SIMI
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ATP-binding; Phosphorylation;
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Best Local
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Hellyer N.
Submitted
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Bumaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                             Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbinert St., Miller M.L., Frohnert P.W., Kim S.S., Corbined Frohners, and their putative receptors, ErbB3, is induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997).
-i- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND IS ACTIVATED BY NEUREGUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 922-1097 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Sciatic
MEDLINE-97184212; PubMed-9030624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hellyer N.J., Kim H.-H., G
"Cloning of the rat ErbB3
recombinant protein.";
Gene 165:279-284(1995).
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MEDLINE-96096535; PubM
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                                SUBCELLULAR LOCATION: Type I membrane protein.
DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR M.
DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR M.
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION
AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBU
PHOSPHATIDYLINOSITOL 3-KINASE.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                      SUBUNIT: HET (POTENTIAL).
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31; Conservative
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N.J., Koland
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535; PubMed-8522190;
Kim H.-H., Greaves C.H
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Sciurognathi; Muridae;
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; Murinae; Rat
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tors, ErbB2 an
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DOMAIN
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SMART; SM00215; FU; 5.

SMART; SM00219; FYIKC; 1.

PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
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InterPro;
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pfam; pF00757; Furin-like; 1.
pfam; pF01030; Recep_Ldomain;
pRINTS; pR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U29339; AAC28498.2; -.
EMBL; U52530; AAC5350.1; -.
HSSP; P11362; 1FGK.
InterPro; IPR000494; EGFR_L_domain.
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 127; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPRO00719; Euk_pkinase.
IPRO02174; Furin-like.
IPRO01245; Tyr_pkinase.
                                                            414
437
469
522
566
516
1028
1339
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1028
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ATP (BY SII
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ATP (BY SII
ATP (BY SIII
ATP (BY SIIIIAR
BY SIMILAR
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                              Score 658;
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CYTOPLASMIC (POTENTIAL).
CYS-RICH.
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101;
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Indels
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RESULT 11
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InterPro; IPRO0
InterPro; IPRO0
InterPro; IPRO0
InterPro; IPRO0
Pfam; PF00069;
Pfam; PF00757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990
16-OCT-2001
15-JUN-2002
                                                                InterPro;
InterPro;
                                                                                           PIR; :
                                                                                                                                                                                                                                                                                             Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                               use by non-profit institutions as long a
modified and this statement is not removed:
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-90015140; PubMed-2797166;
Wittbrodt J., Adam D., Malitschek B.,
Telling A., Robertson S.M., Schartl M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xiphophorus maculatus (Southern platyfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; i
Actinopterygii; Neopterygii; Peleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherin
Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                    "Novel putative receptor tyrosine kinase inducing Tu locus in Xiphophorus."; nature 341:415-421(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor
                                                                                                                      EMBL;
                                                                                                                                                                                                                between
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P13388;
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                                                                                ....0891; CAA34770.2;
R; S06142; S06142.
P; P11362; 1FGK
                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the El European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                   tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANCMAS
                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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                    J IPRO00494; EGFR_L_domain
J IPRO00719; Euk_pkinase.
J IPRO027174; Furin-like,
J IPR002290; Ser_thr_pkinase.
J IPR001245; Tyr_pkinase.
             pkinase;
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Ser_thr_pkinase.
                                                                EGFR_L_domain.
Euk_pkinase.
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                                                                           CWAPGPGHCQKFTKLLCAEQCNRRCRGPKPIDCCNEHCAGGCTGPRATDCLACRDFNDDG
                                                                                                                                                                                 CWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHENHSG
                                                                                                                                                            VLIAMNEVSTIPLVNLRLIRGQNLYEGNETLLVMSNYQK-NPSSP--DVYQVGLKQLQLS
                                                                                                                                                                                                                                            KVCQGTSNQMTM----LDNHYLKMKKMYSGCNVVLENLEITYTQENQDLSFLQSIQEVGGY
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SM00219; TyrKC; 1.
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N_KINASE_DOM; 1.

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Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayrakcaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
Ab Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Buttis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Ab Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subdomains of the receptor protein."; Genetics 137:531-550(1994).

EVISIONS
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13-AUG-1987 (Rel. 05, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Epidermal growth factor receptor precursor (EC 2
(Gurken receptor) (Torpedo protein) (Drosophila
EGFR OR TOP OR C-ERBB OR DER OR CG10079.
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Eukaryota; Metażoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                          STRAIN-Berkeley;
MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Lesokhin A.M., Yu S.-Y., Katz J., Baker N.
"Several levels of EGF receptor signaling
specification in wild-type, Ellipse, and r
Dev. Biol. 205:129-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schejter E.D., Segal D., Glazer L., Shilo "Alternative 5' exons and tissue-specific Drosophila EGF receptor homolog transcript cell 46:1091-1101(1986).
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40:599-607(1985).
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S.-Y., Katz J..
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homolog: conservation of both
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of ERBB)
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA McFulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA McBloon D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Myors E.W., Rubin G.M., Venter T.,
RN The genome sequence of Drosophila melanogaster.";
RN [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Dackwanryeong;
MEDLINE-85137938; PubMed-2983232;
Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
"A Drosophila genomic sequence with homology to human epidermal growth factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- CATALYTIC ACTIVITY: ATP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF receptor.";
Cell 89:13-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perrimon N., Perkins L.A.; "There must be 50 ways to rule the signal: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Raz E., Schejter E.D., Shilo B.Z.;
*Interallelic complementation among the mechanism of signal transduction Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97248481; PubMed=9094709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92038942; PubMed-1936959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1133-1137; 1155-1167 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 959-1078 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 314:178-180(1985).
                                                                  ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II
TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARV
UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGE
TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHE
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADDLIS EXPRESSION IS HIGH IN BRAIN CORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RA MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS. CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE COCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMNIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERN BAND RETRACTION, CELL FA SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
   AND THORACIC AND ABI
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE
MEMBRANE PROTEINS. ISOFORM TYPE III
AND ABDOMINAL GANGLIA.
BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DER/flb alleles: implications for by receptor-tyrosine kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1209-1216 FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine -
                                                                                                                                                                                                                                                                                                                                                                                                     AND TYPE II ARE TYPE S A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            case
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                             IN LARVAE
                                                                                                                                                                                                                                                                                                                               TYPE II AND
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                                                                                                                                                                                                                     ANLAGEN OF
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                                                                                CORTEX
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Best Local S
Matches 110
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EMBL; K03417; AAA51460.1; --
EMBL; K03418; AAA509651; --
EMBL; K03418; AAA5096513; --
EMBL; AF109077; AAD26132.1; --
EMBL; AF109078; AAD26132.1; --
EMBL; AF109078; AAD26133.1; --
EMBL; AF109078; AAD26133.1; --
EMBL; AF109081; AAD26133.1; --
EMBL; AF109081; AAD26133.1; --
EMBL; AF109081; AAD26131.1; --
EMBL; AF109080; AAD26135.1; --
EMBL; X78918; CAA555521.1; --
EMBL; X78918; CAA555521.1; --
EMBL; X78919; CAA555522.1; --
EMBL; X78919; CAA555522.1; --
EMBL; X78919; CAA555522.1; --
EMBL; X78919; CAA55522.1; --
EMBL; X78919; CAA552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0003731; I
Interpro; IPR000494; EC
Interpro; IPR000719; Ev
Interpro; IPR002174; Ev
Interpro; IPR0021745; Ty
                                                                                                                                                                                                                  BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Receptor; P
Tyrosine-protein kinase; ATP-binding; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0109; TYRKINASE.
PYODOM; PD000001; EUK_PKINASE;
SMART; SM00261; FU; 7.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                       Tyrosine-protein
Developmental pro
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; pF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain
                                                                                                                                                                                                                                                                              NP_BIND
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160
                                                                      100
                                  62 YVLIAHNQVRQVPLQRLRIVRGTQLF----
                                                                                                           w
                                                                     AF052754;
AF052753;
AF052754;
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                        869
890
938
944
971
1063
                                                                                                                                               Conservative
                                                                                                                                                                                                                 1 protein:
1 30
31 1426
1 868
9 889
9 1426
1198
952
971
1063
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AAC08535.1; AAC08535.1;
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Euk_pkinase.
Furin-like.
                                                                                                                                                                 33.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Egfr.
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                                                                                                                                             Score 535; DB pred. No. 1.6e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED
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                                                                                                                                                                                                                                        ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                      PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                     EPIDERMAL GROWTH FACTOR RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                  -EDNYALAVLDNGDPLNNTTPVTGASPGGL
                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation; Tr
Signal; Alternative
                                                                                                                                                                 DB 1;
.6e-37;
                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                             116;
                                                                                                                                                                                Length 1426;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase;
ve splicing;
                                                                                                                                             Gaps
                                  116
203
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LT23_CT 13
LT23_C
AC P24348
DT 01-MAR
DT 01-MAR
DT 15-JUN
DE Let-23
GN LET-23
GN LET-23
GN CAENOR
OX CAENOR
OX NCBLT
RN 101
RP SEQUEN
RX MEDLIN
RA AFOLAN
RT CHOMAN
RY MEDLIN
RA SAKAI
RY GENOM
RY MEDLIN
RA SAKAI
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RY SEQUEN
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P24348;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence)
15-JUN-2002 (Rel. 41, Last annotat)
Let-23 receptor protein-tyrosine k
LET-23 OR KIN-7 OR ZK1067.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aroian R.V., Les G.M., Sternberg P.W.;
"Mutations in the Caenorhabditis elegans let-23 elements important for cell-type specificity and EMBO J. 13:360-366(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-96177760; PubMed-8604137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristol N2; Thomas K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sakai T., Koga M., Ohshima 
"Genomic structure and 5' ; the nematode C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91080919;
Aroian R.V., Koga
                                                                                                                                                                                                                                                                                  MEDLINE-99287744; PubMed-10359617; Whitfield C.W., Benard C., Barnes T., Hekimi S., Kim S.K.; Whitfield C.W., Benard C., Barnes T., Hekimi S., Kim S.K.; Benard C., Barnes T., Hekimi S., Kim S.K.; Whitfield C.W., Benard C., Barnes T., Hekimi S., Kim S.K.; Whitefield C.W., Kim S.K.; Waller C., Waller
                                                                                                                                                                                                                                                                                                                                                       STRAIN-Bristol N2;
MEDLINE-99287744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94147981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        induction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOL.
                                                                                        FUNCTION: Tyrosine kinase receptor required fo vulval differentiation. Possible receptor for required for vulval development. Activated by way of let-60 RAS. The lin-3/let-23 pair is a of the mammalian neuregulin-ERBB network.

CATALYTIC ACTIVITY: ATP + a protein tyrosine -
  tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
apical membrane of cell junctions in epithelia.
cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an R.V., Koga
let-23 gene
                                                                                                                                                                                                                                         Biol. Cell 10:2087-2100(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNEFDEAVSKEECPPMRKYNPTTYVLETNPEGKYAYGATCVKECP-GHLLRDNGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348:693-699(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAR-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed-1979659;
M., Mendel J.E., Ohshima Y., Sternucky
necessary for Caenorhabditis elegans vulval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8313880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    б
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a simplified version
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SMART; SM00261; FÚ; 6.
SMART; SM00219; TyrKC; 1
PROSITE; PS00107; PROTEI
PROSITE; PS00109; PROTEI
PROSITE; PS50011; PROTEI
ACT SITE
DISULFID
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modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: Vulval precursor cells.
DEVELOPMENTAL STAGE: Expressed during L2 and L:
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S13422; S13422.
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D63426; BAA09729.1;
Z70038; CAA93882.1;
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 0107; PROTEIN_KINASE_ATP; 1.
0109; PROTEIN_KINASE_TYR; 1.
0011; PROTEIN_KINASE_DOM; 1.
Tyrosine-protein kinase; Develophosphorylation; Transmembrane;
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Euk_pkinase.
Furin-like.
Tyr_pkinase.
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POTENTIAL.
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Y SIMILARITY).
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nbrane; Glycoprotein; Receptor;
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002466;

01-NOV-1997 (Rel. 3

01-NOV-1997 (Rel. 3

15-JUN-2002 (Rel. 4

15-JUN-2002 (Rel. 4
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CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                               )02466;
)1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Insulin-like peptide receptor precursor (EC 2.7.1.112) (ILP receptor).
Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
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VARIANT
SEQUENCE
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VARIANT
VARIANT
                                                                                                                                                                         "Structure and expression of the insulin-like amphioxus.";
                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-96408719; Puby Pashmforoush M., Chan
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TYPOSINE PHOSPHATE.

SUBUNIT: PROBABLE TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN (BY SIMILARITY).
                                                                                                FUNCTION: THIS RECEPTOR BINDS TO THE INSULIN HAS A TYROSINE-PROTEIN KINASE ACTIVITY. CATALYTIC ACTIVITY: ATP + a protein tyrosine
                                                                                                                                                           Endocrinol. 10:857-866(1996).
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N-LINKED (GLCNAC..
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Pred. No. 8e-2
54; Mismatches
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-> Y (IN SY11).

-> I (IN SY16).

-> E (IN SY7).

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Query Match
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Matches 92
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DOMAIN
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the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1]
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00060;
SMART; SM00261;
SMART; SM00219;
                                                                                                                                                                                                                                                                                                                                                                                          pfam; pF000757; Furin-like; 1.
pfam; pF01033; Recep_L_domain;
pRINTS; pR00014; FNTYPEIII.
pRINTS; pR00109; TYRKINASE.
proDom; pD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                               PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S83394; AAB50848.1;
P06213; 1IRK.
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          Similarity
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IPR002011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000494;
IPR000719;
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PROTEIN_KINASE_TYR; 1.
RECEPTOR_TYR_KIN_II; 1.
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Furin-like.
RTKinaseII.
          19.9%;
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FN_III.
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          Score 315.5;
Pred. No. 6.
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ATP
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                                                                                                                                                                                                                                                                                                                         kinase; Receptor; Transmembrane;
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                   BB
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                                                                                                                                                                                                                                                                                                                Signal
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Conservative

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        riterPro; IPR001245; Tyr_pkinase.
Pfam; pF00041; fn3; 1.
Pfam; pF00069; pkinase; 1.
Pfam; pF00757; Furin-like; 1.
Pfam; pF01030; Recen ' '
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Q25197;
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01-NOV-1997 (Rel. 35, I
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Putative insulin-like p
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InterPro; IPR002011;
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Hydridae; Hydra.
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida;
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                                                                                                                                                                  tities requires a license agreement (S send an email to license@isb-sib.ch).
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                                                                                                                                                                                                  European Bioinformatics Institute. There by non-profit institutions as long as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GASCVTACPYNYLSTDVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLAFPNLVEITDYFLLYRVRGLTNLSELFPNLAVIRGTNLF-FNYALVVFEMLD-----
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                                                                                              IPR000719;
IPR003961;
                                                                                                                     IPR000494; EGFR_L_domain
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272
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                                                                                                                                                               QGCQVVQGNL---ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPL-QRLRIVRGTQ 85
                 GICELHCPALVTYNTDTF - - - ESMP - - -
                                   KQQNKAQCQRFCNTQC--GPEGCLDGSDHICCHHECLGGCSAINSTNTCHACRKYRIKST
                                              --ESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSD-CLACLHF--NHS
                                                                                                          LIL-NYALVIYYN-
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GQCVSKCPR-KQYLVDKFLCQESCPYWSINSTEYHHYLWQGECVTKCPVNYISNN
                                                                                       ILWKDI---FHKNNQLALTLIDTNRSRA-----
                                                                      IRWKSIIKDIHQTGQYGIYL-ESNKLNCDLGCLKGHCHPAPGHDGDP--KAQYCWGPGPK
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SM00261;
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87; Conserv
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1002
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PROTEIN_KINASE_TYR;
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1201
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300
325
457
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874
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29.5%;
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Pred. No. 2.4e
32; Mismatches
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                 286
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Search completed: April 28, 2003, 13:40:12 Job time: 14.041 secs

GLEN HINTO SCHOOL SHILL

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Post-processing: Minimum Match 0%
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1587
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1: sp_archea:*
2: sp_bacteria
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                  sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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Q9BG66
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018735
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3080.404 Million cell updates/sec
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                                                                               O9uk79 homo sapien
O18735 canis famil
O90836 gallus gall
O9bg66 oryccolagus
O9erv6 mus musculu
O9ep98 mus musculu
O9ep98 mus musculu
O9ep70 rattus norv
Q9bud7 homo sapien
Q9yh40 xiphophorus
Q9ysh2 gallus gall
P79754 fugu rubrip
Q9bih9 anopheles
Q9w6f6 gallus gall
Q9bg64 oryctolagus
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                                                                      Q9qx70 rattus norv
Q9ese0 rattus norv
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                                          Matches
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                      Doherty J.K., Bond C., Jardim A., Adelman J.P., Clin' "The HER-2/neu receptor tyrosine kinase gene encodes autoinhibitor.";
                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Q9UK79
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99415951; PubMed=10485918;
                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                 Herstatin.
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016131 caenorhabd	016131	σ	18	11.7	185	•
9	5 Q968Y9	ω	184	11.7	185	
anoj		-	1		189	_
Q9n0k4 sus scroft	_			12.0	191	
Q9vfe2 drosophila			æ	•	205	
Q9vj0% drosophila	О		9	•	206.5	
©9ygh8 scophthalmu			12	•	218.5	
			4	•	228.5	
Q63720 rattus			4	14.4	228.5	
			13	•	232.5	
Q8uw85 paralichthy			13	•	244	
			13	•	250	
Q8uw86 paralichthy			13	15.9	252.5	
Q.	Ø		21	•	255	
			1362	16.2	256.5	
٠			14		259.5	
Ð	O		1749	16.9	268	
Q8uw83 paralichthy	13 Q8UW83		14	•	271.5	
O93457 scophthalmu	13 093457		14	17.1	271.5	
Ψ				17.2	273.5	
Q9u5a8 bombyx mori			14		287.5	
Q9njv5 biomphalari			16		289	
Q9y1x8 ephydat			11		317	
Q26568 schistosoma			ω		331	
Q26567 schistosoma			ω		331	
Q26566 schistosoma			17	٠	341	
Q26569 schistosoma	Q26569		366	21.5	341	
_			13		377	
Q9bg65 oryctolagus			_		395	

ALIGNMENTS

PRELIMINARY;

419 ₹

Created)
Last sequence update)
Last annotation update)

Euteleostomi;

Adelman J.P., Clinton G.

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Best Local Similarity
                                                                                                                                                        InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 1.
SMART; SM00261; FU; 1.
                                                                                                                                                                                                                                             Doherty J.K., Clinton G.M., Submitted (SEP-2000) to the EMBL, AF177761; AAD56009.2;
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999).
   22
STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 60
                                                                      Conservative
                                                                                                                                           AA;
                                                                                                                                           45472 MW;
                                                                   100.0%; S
100.0%; P
tive 0;
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                                                                    Score 1587; DB 4;
Pred. No. 2.6e-142;
; Mismatches 0;
                                                                                                                                         FEC1BE347E2D030C CRC64;
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R InterPro; IPR000494; EGFR_L_domain.

R InterPro; IPR0002174; Furin-like.

R InterPro; IPR0002174; Furin-like.

R InterPro; IPR0002174; Furin-like.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR004019; YLP_motif.

R Pfam; PF00757; Furin-like; 1.

R Pfam; PF00069; pkinase; 1.

R Pfam; PF001030; Recep_L_domain; 2.

R Pfam; PF001030; Recep_L_domain; 2.

R Pfam; PF002757; YLP; 2.

R Pfam; PF002757; YLP; 2.

R Pfam; PF00219; TyrKc; 1.

R SMART; SM00219; TyrKc; 1.

R PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00107; Transferase; Tyrosine-protein kinase.

W ATP-binding; Transferase; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               018735;
018735;
01-JAN-1998
01-JAN-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                "cDNA cloning of erbB-2 from Submitted (OCT-1997) to the EMBL; AB008451; BAA23127.1; HSSP; P11362; IFGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9615;
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YVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQL
                                                                                                             TQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQG
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                                                YVLIAHSQVRQIPLQRLRIVRGTQLFEDNYALAVLDNGDPLEGGIPAPGAAQGGLRELQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
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                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          from canine mammary gland.";
the EMBL/GenBank/DDBJ databases
                                                                                                                                            Score 1450; pb ., pred. No. 1e-128;
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Last sequence up
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                                                                                                                                                                      Length 1259;
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Canis.
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RESULT Q9BG66 ID Q9 AC Q9 DT 01 DT 01

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Q9BG66 Q9BG66; 01-JUN-2001 01-JUN-2001

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SEQUENCE
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01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-92123214; PubMed-1732751;

Plickinger T.W., Maihle N.J., Kung H.-J.;

Pan alternatively processed mRNA from the avian can alternatively processed the receptor that can soluble, truncated form of the receptor that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-ERBB.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chor
                                                                                                                                                                                                                                                                                  InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
SMART; SM00261; FU; 2.
                                                                                                                                                                                                                                                                                                                                   dependent transformation.";
Mol. Cell. Biol. 12:883-893(1992).
EMBL; M77637; AAA48759.1; -.
                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF/TGF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q90836
                                                                                                                                                                                                                                                                          Receptor;
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 268
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GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                                      SLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID-TNRSRACHPCSFMCKGS
                                                                                                                     ICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                                                                               RLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PLTVLDFASNLSSCPKCHPNCTED
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527 /
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(TrEMBLrel. 01, Last sequence up
(TrEMBLrel. 21, Last annotation
ha receptor precursor.
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                              AA;
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527
· 58353
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                                                                                                                                                                                                              46.6%;
                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                     48;
                                                                                                                                                                                                    Score 739; DB 13;
Pred. No. 1.1e-61;
8; Mismatches 90;
                                                                                                                                                                                                                                           POTENTIAL.
EGF/TGF-ALPHA RECEPTOR.
; 764564ABCC095298 CRC64;
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Q9ERV6;
Q9ERV6;
Q1-MAR-2001 (TrEMBLrel. 10
01-MAR-2001 (TrEMBLrel. 10
01-JUN-2002 (TrEMBLrel. 10
                                     InterPro; IPRO0
InterPro; IPRO0
Pfam; PF00757; I
Pfam; PF01030; I
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                    Submitted (JUN-2000) to the EMBL; AF275366; AAG28046.1; EMBL; AF275364; AAG28046.1; EMBL; AF275365; AAG28046.1; MGD; MGI:95294; Egfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; C
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2001) to the EMBL EMBL, ARK14371.1; -. EMBL, ARK1471.4; Futin-like. Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "ErbB genes and epidermal growth peri-implantation rabbit uterus a submitted (JAN-2001) to the EMBL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetens F., Fischer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel 18, Last Receptor tyrosine kinase ErbB2 (F
                                                                            InterPro; IPR000345; CytC_heme_bind
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                  Maihle N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                      isoforms."
                                                                                                                                                                                                                                                                                *Comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFESMPNPEGRYTFGASCVTACPYNYLST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPQFCYQDTILWQEFSTRTTSWPSTRINASRARTCPPCSPACQASGCWGESPEDCQSLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFESMPNPEGRYTFGASCVTTCPYNYLST
                                                                                                                                                                                                                                                           alternative
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Similarity 81.2%;
21; Conservative
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ative Egfr transcripts
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Recep_L_domain; 2.
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Rodentia;
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16, Last
21, Last
receptor
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                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 723; DB Pred. No. 7.5e B; Mismatches
                                                                                                                                                                                                                                                       analysis and ripts encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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annotation update)
isoform 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation
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ae; Oryctolagus
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7.5e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EGF-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₿
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                                                                                                                                                                                                                                                                                                                     K.E:, Danielsen F
, Lampland A.L.,
, James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-LIVER; Reiter J.L., Threadgill D.W., Da. Lampland A.L., Balasubramaniam c Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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SEQUENCE FROM N. D.

STRAIN-C57BL/6J; TISSUE-LIVER;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217860;

MEDLINE-2108660; PubMed-11217860;

MEDLINE-210866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                       Carboxy-Terminal Truncated I Submitted (JAN-1999) to the
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                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                           mouse
                                                                                                                                                                                                                                                                                                  Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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138; Conser
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Rodentia;
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47.3%;
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QDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGS
                                                                                                                                                          NLQEILIGAVRESNNPILCNMDTIQWRDIVQNVFMSNMSMDL
            NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                                                                                                          SLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLIDTNRSRACHPCSPMC
                                                                                                                                           VLIALNTVERIPLENLQIIRGNALYENTYALAILSN------YGTNRTGLRELPMR
                                                                                                                                                                                                                                                                                                                   CYTOCHROME_C;
                                                                                                                                                                                                                                                       Score 716.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                            DEF22002C84911B1 CRC64;
                                                                                                                                                                                                                                            Mismatches
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                                                                                             --- QSHPSSCPKCDPSC
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 306
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STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D.,
Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                     "Alternative Transcripts from the
                          genomic sequence analysis ative Egfr transcripts enco
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12, Last
21, Last
receptor
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Receptors.";
e EMBL/GenBank/DDBJ
EMBL/GenBank/DDBJ
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m S., Cross
                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
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annotation update)
(Epidermal growth
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                                                                                                                                                                                                             J., Schell
/ T.O., Mag
                                           isolation
                                                                                                                                                                                       Mouse
                            truncated
databases
                                                                                                K.E.,
                                                                    K.E., Danielsen A
, Lampland A.L.,
, James C.D.,
                                                                                                                                                                                     EGFR
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Murinae; Mus
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                                           of human
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J., Fukuda S., Yamanaka I T., Saito F

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RESULT

Q9EP98

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Best Local S
Matches 138
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EMBL; AF224513; AAD24149.1; -
EMBL; AF275366; AAG28047.1; JOINED.
EMBL; AF275365; AAG28047.1; JOINED.
EMBL; AF275365; AAG28047.1; JOINED.
EMBL; AF004944; BAB23688.1; -
EMBL; AK004944; BAB23684.1; -
EMBL; AK004911; BAB23662.1; -
MGD; MGI 95294; Egfr.
                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=10090;
                                                                                                                                                                             O9EP98;
01-MAR-2001 (TrEMB
01-MAR-2001 (TrEMB
01-JUN-2002 (TrEMB
Epidermal growth f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J. Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T. Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F. Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., unanchiraki Y.
STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC; Reiter J.L., Threadgill D.W., Eley G.D., Sinclair C.S., Pearsall R.S., Green P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
Pfam;
                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                  Q9EP98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:95294;
InterPro; IPROO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
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rPro; IPR002174; Furin-like.
PF00757; Furin-like; 1.
PF01030; Recep L. Ammi-
                                                                                                                                                                                                                                                                                                                                                                                                                   NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLIDTNRSRACHPCSPMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSELQDIQEVQGY
                                                                                                                                                                                                                                                                                                                                                                                             QDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAGCTGPRESDCLVCQKF
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                                                            FROM N.A.
                                                                                                  ıs (Mouse).
Metazoa; Chordata; C
¬…+heria; Rodentia; {
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
rowth factor receptor isoform 1.
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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47.3%; Pred. No. 1.9e-59;
tive 39; Mismatches 96;
                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Strunk
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Lampland
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Q9Qx70;
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Query Match
Best Local
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Interpro; IPR000349; EGFR_L_domain.
Interpro; IPR0002174; Furin-11ke.
Interpro; IPR0022174; Furin-11ke.
Interpro; IPR0022174; Furin-11ke.
Interpro; IPR002230; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001030; Recep_L_domain; 2.
Pfam; PF00059; Pkinase; 1.
Pfam; PF001030; Recep_L_domain; 2.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; TyrKC; 1.
SMART; SM00210; TyrKC; 1.
PROSITE; PS00119; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00119; PROTEIN_KINASE_DM; 1.
PROSITE; PS00119; PROTEIN_KINASE_TYR; 1.
ATP-binding; Receptor; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF275366; AAG2804
EMBL; AF275364; AAG2804
EMBL; AF275365; AAG2804
EMBL; AF275365; AAG2804
EMBL; AF275367; AAG2438
HSSP; P11362; IFGK.
MGD; MGI:95294; Egfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J;
STRAIN-C57BL/6J;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., D
Reciter J.L., Pearsall R.S., Green P.J., Yee D., Lampland
Schehl C., Pearsall R.S., Grossley T.O., Magnuson T.R., James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative genomic sequence analysis and isolation of human mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                   VLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR
QDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGS
                                                                                                                                                                        SLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLIDTNRSRACHPCSPMC
                                                                                                                                                                                                                              VLIALNTVERIPLENLQIIRGNALYENTYALAILSN-----YGTNRTGLRELPMR
                                 NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                                                                         PNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAGCTGPRESDCLVCQKF
                                                                                             KGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
                                                                                                                                                    NLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL----QSHPSSCPKCDPSC
                                                                                                                                                                                                                                                                                                                                                                                   138;
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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; AAG28045.1;
; AAG24386.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          134840 MW;
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                                                                                                                                                                                                                                                                                                                                                                                   39;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 716.5; DI
Pred. No. 4e-59;
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                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   96;
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npland A.L.,
, James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
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306
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Best Local
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01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                               Guttridge K., Dawson T.L., E submitted (NOV-1999) to the EMBL; M37394; AAF14008.1; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                            PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                            PRINTS: PRO0109; TYRKINASE.
Probom: PD000001; Euk_pkinase;
SMART; SM00251; FU; 3.
SMART; SM00219; TYIKC; 1.
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00757; Furin-like; 1. Pfam; PF00069; pkinase; 1. Pfam; PF01030; Recep_L_domain;
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InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-FISHER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                      VLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR
                                                                                                                                                                              QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGY
ATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGS
                 GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                                                   RCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
                                                                                              SLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRS-RACHPCSPMCKGS
                                                                                                                            VLIALNTVERIPLENLQIIRGNALYENTYALAVLSN------YGTNKTGLRELPMR
                                                                                                                                                                   KVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGY
                                                                                 NLQEILIGAVRFSNNPILCNMETIQWRDIV-QDVFLSNMSMDVQRHLTGCPKCDPSCPNG
                                        SCWGRGEENCQKLTKIICAQQCSRRCRGRSPSDCCHNQCAAGCTGPRESDCLVCHRFRDE
                                                                                                                                                                                                                al Similarity
137; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOV-1991) to the
                                                                                                                                                                                                                                                        i; Receptor; Transferase; Tyrosine-protein kin
1209 AA; 134891 MW; 96FEE7F6CC1B7773 CRC64;
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LIVER;
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                                                                                                                                                                                                                          44.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13, Created)13, Last sequence upo21, Last annotation or receptor.
                                                                                                                                                                                                                41;
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                                                                                                                                                                                                              Score 708.5;
Pred. No. 2.36
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
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Sciurognathi;
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Submitted (MAR-2001) to the EMBL/GenE
EMBL; AF187818; AAG17037.2; -
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR0002174; Furin-like, 1
Pfam; PF00757; Furin-like; 1
Pfam; PF01030; Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9ESEO, PRELIMINARY;
O9ESEO;
01-MAR-2001 (TrEMBLrel. 1
01-OCT-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                  SEQUENCE FROM N.P
TISSUE-PLACENTA;
Strausberg R.;
                                                                                                                                                                                                                                           Receptor.
SEQUENCE
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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   Submitted (FEB-2001) to the EMBL/Ge EMBL; BC002706; AAH02706.1; -. InterPro; IPR000494; EGFR_L_domain. InterPro; IPR0002174; Furin-like.
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Yu Y., Moshier J.A., Majumdar A.F
"Cloning of a novel EGFR-related
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                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Sciurognathi; Muridae
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Catarrhini;
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                                        Pfam; PF01030; Recep_L_domain; PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                         Submitted (JUL-2000) to t
EMBL; U53471; AAD10500.2;
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                           Schartl M.;
Submitted (
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Activation of the Xmrk proto-oncogene of xiphophorus overexpression and mutational alterations."; Oncogene 16:1681-1690(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98241172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock
Altschmied J., Schartl M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-RIO PURIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Verte Actinopterygii; Neopterygii; Teleostei; Eutel Acanthomorpha; Acanthopterygii; Percomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-RIO PURIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                        InterPro;
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                                                                                                                                        InterPro;
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                                                                  PF01030;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGHNADLSFLQWIREVT
                                                                                                         Pro; IPR000719; Euk_pkinase.
Pro; IPR002174; Furin-like.
Pro; IPR001899; Gram_pos_anchor
Pro; IPR001245; Tyr_pkinase.
Pr00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFV
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SM00261;
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                                                                                                                                                                                                                                IPR000494;
                                                                                                                                                                                                                                                      IPR000345; CytC_heme_bind
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Recep_L_domain;
                   Euk_pkinase;
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36489 MW;
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Euteleostei; Neoteleostei
rpha; Atherinomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gomez A.,
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PROSITE; PS00190; CYTCOCHROME_C; UNKNOWN_1.

PROSITE; PS00143; GRAM_POS_ANCHORING; UNKNOWN_1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 2.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.

ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.

SEQUENCE 1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-94020816; PubMed-8414496;
Callaghan T., Antozak M., Flickin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Fragment).
Epidermal growth factor receptor (Fragment).
Equipment (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR000494; EGFR_L_domai InterPro: IPR002174; Furin-like. Pfam; PF00757; Furin-like; 2. Pfam; PF01030; Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 8:2939-2948(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kung H.J.;
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                                                                                                      KVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLEITYVEHNRDLTFLKTIQEVAGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CWAPGPGHCQKFTKLLCAEQCNRRCRGPKPIDCCNEHCAGGCTGPRATDCLACRDFNDDG
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127; Conserv
                                                                                                                                                                                                                                                                                                                         SM00261; FU;
CE 599 AA;
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         66363 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGFR_L_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flickinger T.,
                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                             Score 635.5; DB 13
Pred. No. 8.3e-52;
8; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 649.5; DB 13; Pred. No. 8.7e-53;
                                                                                                                                                                                                                                                                                                                         FEAB46D293D991BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raines
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                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                             Gaps
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                                                                                                                                                   Query Match
Best Local S
Matches 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P79754 PRELIMINARY;
P79754;
01-MAY-1997 (TrEMBLrel. 0
01-MAY-1997 (TrEMBLrel. 0
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain; 2.
ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                               SMART; SM00261; FU; 3. SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                    ATP-binding; Transferase.
SEQUENCE 1328 AA; 148613 MW; A333039258B647E9
                                                                                                                                                                                                                                                                                                          PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Futin-1ike.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF056116; AAC34391.1; HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 9:251-258(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rubripes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gellner K., Brenner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-99177347; PubMed-10077531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acanthomorpha; Acanthopterygii; Percomorpha;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415
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        64
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                                                                                              VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHCWGAGEONCOTLTKVICAQQCSGRCRGKVPSDCCHNQCAAGCTGPRESDCLACRKFRD 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNH 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRSLKEISDGDIAIMKNKNLCYADTMNWRSLFATQSQKTKIIQNRNKNDCCPKCHPNCTE
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LIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRS
                                                   VCPGTQNGLSSTGSQENQYNLNKDRYKGCEIIMGNLEITQIESNWDFSFLKTIREVTGYV
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                                                                                                                                                   al Similarity 42.1
119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 148 kb of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                      37.6%; Score 596.5;
42.3%; Pred. No. 1.16
tive 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic DNA around the wntl locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03, Created)
03, Last sequence update)
21, Last annotation update)
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                                                                                                                                                      1.1e-47;
ches 105;
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                                                                                                                                                      Indels
                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Fugu
                                                                                                                                                      15;
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                                                                                                       Query Match
Best Local S
Matches 113
                                                                                                                                                                                                  Pfam; PF01030; Recep_L_domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 7.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; TYFKC; 1.
SMART; SM00219; TYFKC; 1.
SMART; SM00219; TYFKC; 1.
PROSITE; PS00110; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                           Receptor.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                         Pfam; PF00757; Furin-like; 1. Pfam; PF00069; pkinase; 1. Pfam; PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, expression and localisation of the Anopheles gambiae epidermal growth factor receptor."; submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota; Neoptera; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last squence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment).
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HSSP; P11362; 1FGK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anopheles gambiae (African malaria mosquito)
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ISLYDLPQVILPRLQIIRGRTTFKLNKWEEAYGLFV-----
                                                   CIGTNGRMSVPANREYHYKNLRDRYTNCTYVDGNLEITWIQNITDLNFLQHIREVTGYVL
                                                                  CTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVPQCPQTLIYNKQTFQMETNPNAKYQYGSICVSQCPTHFV 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WGPGKDQCQILTKTVCAPQCNDRCFGTSPRDCCHIECAAGCKGPLDTDCFACRLFNDSGA
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                        IAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGAS/GGLREL 119
                                                                                                       al Similarity
113; Conser
                                                                                                                                                                                                                                                                                                                                                                                  IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000494; EGFR_L_domain.
                                                                                                                                                                                                                                                                                                                                                                  IPR002290; Ser_thr_pkinase IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                             IPR000719; Euk_pkinase.
IPR002174; Furin-like.
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                                                                                                                  34.2%;
                                                                                                                                                              159585 MW;
                                                                                                        45;
                                                                                                      Score 543; DB 5;
Pred. No. 1.4e-42;
5; Mismatches 109;
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Best Local Similarity
                                                                                                                                                                                           PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00652; THER_NGFR_1; UNKNOWN_1.
KINASe; Tyrosine-protein kinase.
NON_TER 1 1
SEQUENCE 1137 AA; 127927 MW; 4D616436
                                                                                                                                                                                                                                                                                    SMART; SM00261; FU; 3.
SMART; SM00219; TyrKc; 1.
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Pfam; PF0075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1099 (TrEMBLrel. 21, Last annotation update)
Receptor tyrosine kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                        Pfam; PF01030; Pfam; PF02757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Distribution of neuregulin-1 (nrg1) and embryonic chick hindbrain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9W6F6
                                                                                                                                                                                                                                                                                                              PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dixon M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                     [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9031;
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ESMPNPEGRYTFGASCVTACPYNYL 283
                                    AEQCDGRCYGPYVSDCCHRECAGGCSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTF
                                                   AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVG-CWGEGAHNCQRFSKLNCSPQCSQGRCFGPKPRECCHLFCAGGCTGPTQSDCLACKN
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AF121963; AAD31764.1;
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IPR004019; YLP_motif.
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                                                                                                                                           Conservative
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Pred. No. 8.8e-30;
.8; Mismatches 55;
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Db 122 QLEHNHNAKYTYGAFCVKKCPHNFV 146

Search completed: April 28, 2003, 13:41:35 Job time : 23.3311 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1587
1 STQVCTGTDMKT.PT.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                April 28, 2003, 13:39:54; Search time 8.45736 Seconds (without alignments) 1005.423 Million cell updates/sec
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US-08-625-101-2
US-08-625-101-2
US-08-468-5458-68
US-08-356-768-2
US-08-336-708A-9
US-08-336-708A-9
US-08-484-438-4
US-08-484-438-4
US-08-484-438-4
US-08-484-438-2
US-08-484-38-2
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US-08-414-417B-68
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US-09-344-195-4
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                                                                                        Query Match
Best Local Similarity
Matches 289; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application Patent No. 6414130
                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206 628-7621
TELEFAX: 206 628-7699
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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440
 61
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NAME: Davison, Barry L.
REGISTRATION NUMBER: 47,309
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MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Word
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ADDRESSEE: DAVIS WRIGHT TREMAINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Doherty, Joni Kristin and Gail M. TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231.5
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                                              STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
                                STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                    ENT APPLICATION DATA:
APPLICATION NUMBER: US/09,
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                                                                                                 STRANDEDNESS: single
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                                                                                          100.0%;
ilarity 100.0%;
Conservative
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US-09-457-040B-7

US-09-457-040B-7

US-08-746-559A-4

US-08-625-819-2

US-08-625-819-2

US-08-625-819-2

US-08-64-641B-18

US-08-864-641B-18

US-08-857-076-103

US-08-857-076-12

US-08-857-076-104

US-08-857-076-104

US-08-857-076-106

US-08-752-633-1

US-08-752-633-1
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                                                                                          Score 1587; DB 4;
Pred. No. 3.6e-139;
; Mismatches 0;
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Clinton

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18, Appl 5, Appl 103, App 12, Appl 105, Appl 104, App 106, App

Sequence

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Result

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Match Query

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Searched:

262574 seqs,

Database

Title: Perfect score:

Sequence:

Scoring table:

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US-08-422-108-J
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Best Local Similarity
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                                                                                                                                                                                      TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WinPatin (Ge:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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FILING DATE: 13-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                1 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 60
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STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
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                                                              289;
                                                                                                                                                          Amino Acid
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                                                                                                                                                                                                                                                                                                               Lee, Wendy M
                                                                                                                                                                         624 amino acids
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                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         UMBER: 08/048346
15-APR-1993
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                                                           Score 1587; DB.3;
Pred. No. 6e-139;
; Mismatches 0;
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TOPOLOGY:
US-08-422-734-1
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Query Match 100.0%; Score 1587; DB Best Local Similarity 100.0%; Pred. No. 6e-139; Matches 289; Conservative 0; Mismatches
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                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/3
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
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                                                                                           Amino Acid
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19-MAY-1989
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SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS 240

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LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG 180 GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 120

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STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ

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Best Local (
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Patent No. 5976546
                                                    Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                   NAME: Judge, Linda R. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                    Local Similarity
                                                                                                                                 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig.
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 03-SE
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1 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 60
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350 Cambridge Ave. Suite
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                                                                Score 1587; DB 2; Pred No. 8.1e-139;
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1 STOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 60

STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 81

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Best Local S
Matches 289
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                                                                                                                                                                                                                  TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO:
                                                                         ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig.
                                                                                                                       MOLECULE TYPE: pr
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                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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NAME: Judge, Linda R.
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CITY: Palo Alto
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94306
               Local Similarity
                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
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                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0,
   Conservative
                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                         protein
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              100.0%;
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               Score 1587; DB 3; Pred. No. 8.1e-139;
   Mismatches
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                               Length
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Gaps
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                                                                          Query Match
Best Local Similarity
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                                                               Matches
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   22
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
ADDRESSEE: Orambridge Ave. Suite 250
                                                                                                                                       ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig.
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                         TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-199
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu, Hongyu
TITLE OF INVENTION: In
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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Ruegg, Curtis L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 289
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                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/146,283 FILING DATE: 03-SEPT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
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                                                                                                                                                                                                                                                                LENGTH: 782 amino acids
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                                                                          Score 1587;
Pred. No. 8.
                                                              Mismatches
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                                                                          DB 4;
1.1e-139;
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                                                                                                                           Query Match
Best Local S
Matches 289
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                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 68:
                                                                                                                                                                                                                                                                                                                NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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                               61
                                                                                                                                        Local Similarity
                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
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                                                                                                                                                                                                                                      LENGTH:
GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 120
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                                                                           STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 60
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                                                              STOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                        1255 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin A.
                                                                                                                                        100.0%; Score 1587; DB 1; 100.0%; Pred. No. 1.5e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/414,417
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                                                                                                                             Mismatches
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                                                                                                                                                         Length 1255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/414

CLARSTETT US 231-445

COURTENT APPLICATION NUMBER: US/08/414

CLASSTETT US/08/414
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                         61 GYYLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 120
                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                   22 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                   1 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHENHS
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                                                                                                         GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ
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Disis, Mary L.
                                                                                                                                                                                                                              100.0%; Score 1587; DB 1; Alarity 100.0%; Pred. No. 1.5e-138; Conservative 0; Mismatches 0;
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Patent No. 58:
                                            Matches 289;
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LENGTH: 1255 amino acids
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 15M FC DOS/MS-1000
OPERATING SYSTEM: PC-DOS/MS-1000
COFTWARE: Patentin Release #1.0, Version
OPERATING ATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/3
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 0
FILING DATE: 10-NOV-1993
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1 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 60
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Y: U.S.A.
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Culouscou, Jean-Michel
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                                              Conservative
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Hellstr m, Karl E.
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                                                            100.0%; Score 1587; DB 2; 100.0%; Pred. No. 1.5e-138;
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                                              Mismatches
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NAME: Sharkey, Richard G
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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CLASSIFICATION: 424
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06) 682-6031
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Pred. No. 1.5e-138;
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TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1255 amino aci
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                                                                                                                                                                       61 GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ
                                                                                                                                                                                                                                                                                               Local Similarity
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 GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
                               SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
                                                           SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
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98104-7092
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INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
INVENTION: REACTIVITY TO HER-2/neu PROFEIN FOR PREVENTION
INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
INVENTION: ONCOGENE IS ASSOCIATED
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Pred. No. 1.5e-138;
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RESULT 13
US-08-356-786-2
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US-08-468-545B-68
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GENERAL INFORMATION:
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LENGTH: 1255 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Disis, Mary L
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REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92:
TELECOMMUNICATION INFORMATION:
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STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                        GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 120
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5876712
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Pred. No. 1.5e-138;
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Best Local S
Matches 289
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
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                                                                                 SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS 240
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GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
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amino acid
NGY: linear
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State Street
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US-08-466-680B-68 US-08-466-680B-68 ; Sequence 68, Application US/08466680B ; Patent No. 6075122

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                                                                                                                               Sequence 9, Application US/08336708A Patent No. 5521295
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                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 92C
TELECOMMUNICATION INFORMATION:
TRELEBURGE: 7000.
     NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES:
                                                               APPLICANT:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                               SRCWGESSEDCOSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS
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                                                                               Thomason, Arlen R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Recurrent Application Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1
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259 TCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGS
                       242 ICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 289
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                                                                                                                                                   139 NLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNHLGSCQKCDPSCPNGS 198
                                                                                                                                                                                      123 SLTEILKGGVLIQRNPOLCYODTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSR 182
                                                                                                                                                                                                                              89 VLIALNTVERIPLENLQIIRGNMYYENSYALAVLSNYD------ANKTGLKELPMR 138
                                                                                                                                                                                                                                                        63 VLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR 122
                                                                                                                                                                                                                                                                                                        29 KVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGY 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                           CWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSG 241
                                                                           CWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKFRDEA 258
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Pred. No. 2.9e-58;
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Search completed: April 28, Job time: 15.4574 secs 2003, 13:43:18 В Ş В δÃ 밁 δÃ 망 Ş 밁 δ

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Matches
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Result

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US-10-123-155-227	US-10-123-155-509	US-10-123-155-359	US-09-466-320-19	US-09-466-320-11	US-10-123-155-323	US-09-844-353A-106	us-09-205-658-106	US-09-844-353A-104	US-09-205-658-104	US-09-844-353A-105	US-09-205-658-105	US-09-844-353A-12	US-09-205-658-12	US-09-844-353A-103	US-09-205-658-103	US-09-870-759-120	US-10-172-620-17	US-10-172-620-16	US-09-867-521-2	US-09-940-101-4	US-09-940-101-2	US-09-725-433-2	US-10-172-620-18	US-09-441-411-9	US-09-854-356-14
Sequence 227, App	•	359,			323, <i>į</i>	Sequence 106; App	•	104,	104,	Sequence 105, App	•	Serjuence 12, Appl		Sequence 103, App	Sequence 103, App	Sequence 120, App	17,	•	Sequence 2, Appli	4	Sequence 2, Appli	Sequence 2, Appli	Sequence 18, Appl	~	Sequence 14, Appl

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: LAUS, Reiner
APPLICANT: VIdovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Der
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT APPLICATION NUMBER: US 60/193,504
PRIOR APPLICATION WIMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens US-09-821-883-23
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SEQ ID NO 23
LENGTH: 289
TYPE: PRT
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Local Similarity 100.0%;
nes 289; Conservative C
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                                                                                           LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG 180
                                                                       LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG
SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHENHS
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Pred. No. 6.2e-120;
D; Mismatches 0;
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US-09-821-883-5
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                                                                                                                                                                                   GENERAL INFORMATION
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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Patent No. US20020061310A1
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                                                                                      APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Cell-Based I
FILE REFERENCE: 7636-0022.30
            PRIOR APPLICATION NUMBER: US 60/193,504 PRIOR FILING DATE: 2000-03-30 NUMBER OF SEQ ID NOS: 30
                                                         CURRENT APPLICATION NUMBER: US/09/821,883
                                                                                                                                                                 APPLICANT: Laus,
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CURRENT EILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
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TYPE: PRT
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; OTHER INFORMATION: HER500* construct US-09-821-883-3
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US-09-821-883-3
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LENGTH: 564
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APPLICANT: Laus, Re
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
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APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Cell-Based Immunotherapy
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                                                                                               GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 120
                                   LRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKG 180
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Pred. No. 1.3e-119;
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Pred. No. 1.3e-119;
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          APPLICANT: SmithKline Beecham Biologicals S. A. TITLE OF INVENTION: HER-2/new Fusion Proteins FILE REFERENCE: 014058-009810pc CURRENT APPLICATION NUMBER: US/09/854,356 CURRENT FILING DATE: 2001-05-09 PRIOR APPLICATION NUMBER: US 09/493,480 PRIOR APPLICATION NUMBER: US 09/493,480 PRIOR APPLICATION NUMBER: US 60/117,976 PRIOR APPLICATION NUMBER: US 60/117,976 PRIOR APPLICATION NUMBER: US 60/117,976 PRIOR FILING DATE: 1999-01-29
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham
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Best Local Similarity
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SEQ ID NOS:
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Pred. No. 1
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; FEATURE: ; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu US-09-854-356-3
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Best Local S
Matches 289
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Best Local Similarity
Matches 289; Conserv
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TYPE: PRT
ORGANISM: Homo s
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CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Cell-Based Immunotherapy FILE REFERENCE: 7636-0022.30
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APPLICANT: Vidov
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                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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289; Conser
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Graddis, Thomas
                                                                                                                                                                                               100.0%; Score 1587; DB 10; ilarity 100.0%; Pred. No. 1.7e-119; Conservative 0; Mismatches 0;
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APPLICANT: VIGOVIC, Damir
APPLICANT: VIGOVIC, Damir
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 697
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US-09-821-883-4
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          GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
                                                                                                                                                      Sequence 7, Application.US/09854356 Patent No. US20020177567A1
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Best Local Similarity 100.0%;
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Patent No. US20020061310A1
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APPLICATION
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NUMBER: US/09/854,356
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OTHER INFORMATION: Description of Artificial Sequence: fusion : OTHER INFORMATION: of ECD and PD of human HER-2/neu US-09-854-356-6
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Query Match
Best Local Similarity
Matches 289; Conserv
                                                                                                                                                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 6
LENGTH: 919
TYPE: PRT
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APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
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                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 26
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APPLICANT: Corixa Corporation
APPLICANT: SmithKine Beecham Biologicals S.
APPLICANT: HBR-2/neu Fusion Proteins
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PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
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                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/117,976
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SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                       FEATURE:
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Score 1587; DB 9;
Pred. No. 2.4e-119;
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; ORGANISM: HOMO S
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US-09-769-508-2
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                                                  RESULT 12
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Best Local S
Matches 289
    Sequence 1, Application US/09854356 Patent No. US20020177567A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHAO, LORRINE A.
APPLICANT: BLUFORD, PETER
TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
FILE REFERENCE: BEBIO-111-C1
CURRENT APPLICATION NUMBER: US/09/769,508
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: MONAHAN, JOHN J.
APPLICANT: LANGTON, BEATFRICE CLAUDIA
APPLICANT: HANCOCK, MIRIAM E.C.
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Pred. No. 3.4e-119;
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Matches 289
                                                                                          GENERAL INFORMATION:
APPLICANT: Hand-Zim
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APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
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APPLICANT: Corixa Corporation
APPLICANT: Smithkline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
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CURRENT FILING DATE: 2001-05-09
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                                 APPLICANT:
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                   APPLICANT:
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COCATION: (990). (1048)

OTHER INFORMATION: portion (delta PD)
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LOCATION: (990)...(1255)
OTHER INFORMATION: phosphorylation domain (PD)
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ORGANISM: Homo sapiens
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LOCATION: (676)..(1255)
OTHER INFORMATION: intracellular domain (ICD)
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LOCATION: (1)..(653)
OTHER INFORMATION: extracellular domain (ECD)
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OTHER INFORMATION: human HER-2/neu
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Foy, Teresa M.
Lodes, Michael J.
Kalos, Michael D.
McNeill, Patricia [
Vedvick, Thomas S.
                                                                                               Hand-Zimmerman,
                                                                             Cheever, Martin A.
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Helistrom, Ingegerd
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CURRENT FILING DATE: 2001-08-14
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                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Hellstrom, Ingegerd
PPLICANT: Hellstrom, Karl Erik
ITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
ILE REFERENCE: 730033.409
                                                                                                                                                                                                                                                                                      ENGTH: 1255
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                                82 GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ
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Windows Version 4.0
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PRIOR APPLICATION NUMBER: 05/238,327
PRIOR FILING DATE: 2001-03-16
PRIOR PRIOR DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
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TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
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APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowsk
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FILE REFERENCE: GENENT.073A2
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                   241 GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS
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ALIGNMENTS

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A; Molecule type: DNA A; Residues: 832-909					

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A;Residues: 1-144 <MIY>
A;Cross-references: EMBL;X03021; NID:g31858; PIDN:CAA26822.1; PID:g31859
R;Kaushansky, K. O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hagen, F.S.; Av
Proc. Natl. Acad. Sci. U.S.A. 83, 3101-3105, 1986
A;Title: Genomic cloning, Characterization, and multilineage growth-prom
A;Reference number: I59065; MUID:86205844; PMID:3486413
A;Accession: I59065
                                                                                                                                                                                                                                         R;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K. EMBO J. 4, 2561-2568, 1985
A;Title: Structure of the chromosomal gene for granulocyte-macrophage A;Reference number: A91015; MUID:86030234; PMID:3876930
A;Accession: C24636
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C; Accession:
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F;654-675/Domain: transmembrane #status predicted <TMM>
F;654-675/Domain: intracellular #status predicted <INT>
F;676-1255/Domain: protein kinase homology <KINV
F;718-983/Domain: protein kinase homology <KINV
F;726-734/Region: protein kinase ATP-binding motif
F;684,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;753/Active site: Lys #status predicted
F;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
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A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMI
A;Map position: 17q21.1-17q21.1
A;Introns: 25/1; 75/3; 147/1: 883/3
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N;Alternate names: colony-stimulating factor 2; GM-CSF
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                                                                                                                                                                                                                  A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                     Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change;Accession: C24636; I59065; A25169; A01853; A44175; JC1090;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
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     translated
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Pred. No. 6.9e-281;
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p-185 precursor - golden hamster C; Species: Mesocricetus auratus (golder C; Date: 02-Jul-1996 #sequence_revision C; Accession: 148161 R; Nakamura, T.; Ushijima, T.; Ishizaka,
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A;Residues: 1-116,'T:,18-144 <WON>
A;Residues: 1-116,'T:,18-146
A;Cross-references: GB:M10663; NID:g181145; PIDN:AAA52121.1; PID:g181146
A;Cross-references: GB:M10663; NID:g181145; PIDN:AAA52121.1; PID:g181145; PIDN:AAA52121.1; PID:g181146
A;Cross-references: GB:M10663; NID:g181145; PIDN:AAA52121.1; PID:g181146
A;Cross-references: GB:M10663; NID:g181145; PIDN:AAA52121.1; PID:g181145; PIDN:AAA52121.1; PID:g181145; PIDN:AAA52121.1; PID:g181145; PID:g181145; PIDN:AAA52121.1; PID:g181145; PIDN:g181145; PIDN:g181145; PIDN:g181145; PIDN:g181145; PIDN:g181145; PIDN
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R;Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.; Luh, J.; Arai, K.; Re
Proc. Natl. Acad. Sci. U.S.A. 82, 4360-4364, 1985
A;Title: Isolation of cDNA for a human granulocyte-macrophage colony-stimulating
A;Reference number: A01853; MUID:85242684; PMID:3925454
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A;Residues: 1-144 <RES>
A;Cross references: GB:M13207; NID:g181147; PIDN:AAA98768.1; PID:g181148
A;Cross references: GB:M13207; NID:g181147; Price, V.; McKereghan, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: stimulates the differentiation and proliferation of hematopoietic C;Superfamily: granulocyte-macrophage colony-stimulating factor C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell F;1-17/Domain: signal sequence #status predicted <SIG>
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Science 228, 810-815, 1985
A;Title: Human GM-CSF: molecular cloning of the complementary
A;Title: Human GM-CSF: molecular cloning of the complementary
A:Reference number: A44175; MUID:85218749; PMID:3923823
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Proc. Natl. Acad. Sci. U.S.A. 82, 6250-6254, 1985
A;Title: Cloning, sequence, and expression of a human granulocyte/macrophage
A;Reference number: A25169; MUID:85298329; PMID:3898082
A;Accession: A25169
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A;Map position: 5q23.2-5q31.1
A;Introns: 53/3; 67/3; 109/3
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A; Residues: 18-21,'C',23-96,'L',98-144
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A;Accession: JC1090
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A; Accession: A44175
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R;Wong, G.G.; Witek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary,
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A; Residues: 1-144 <CAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 137
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                                                                                                                                                                                                                                                                                                                                                                                                                           CWEPVQE 144
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site: carbohydrate (Asn) (covalent) #status
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100.0%; Pred. No. 6.5e-118;
                                                                                                                                    (golden hamster)
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y, A.C.; Luxenberg,
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Nagao,

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A; Gene:
C; Super:
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                                                                                                                                                  F;723-988/Domain: protein kinase homology <KIN>F;731-739/Region: protein kinase ATP-binding motif F;731,191,263,535,576,634/Binding site: carbohydrate (As F;691/Binding site: phosphate (Thr) (covalent) #status F;758/Active site: Lys #status predicted F;882,1227,1253/Binding site: phosphate (Tyr) (covalent
                                                                                                                                                                                                                                                                                      C;Keywords: ATP; autophosphorylation; duplication; glyof;1-19/Domain: signal sequence #status predicted <SIG>F;20-1260/Product: protein-tyrosine kinase neu #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Bargmann, C.I.; Hung, M.C.; Weinberg, R.A. Nature 319, 226-230, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway ra
C;Date: 31-Dec-1988 #sequence_revision
C;Accession: A24562; A61204
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The neu oncogene encodes an epidermal growth factor receptor-related A;Reference number: A24562; MUID:86118662; PMID:3945311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-tyrosine kinase (EC 2.7.1.112) neu precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status:
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235
                                   250 LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESM 301
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                                                                                                                                                                                                                                                                                                                                                                                                                  authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no lyl]formamide or N-methyl-N-nitrosourea.
nce number: A61204; MUID:92035293; PMID:1682063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary
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LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESM
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637-663,'V'
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kinase ATP-binding motif
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                                                                                                                                                      (Tyr) (covalent) #status
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                                                                                            DB 1; Le 1.3e-42;
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A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Cross-references: EMBL:X52174; NID:g28321; PIDN:CAA36422.1; PID:g28322
A;Cross-references: EMBL:X52174; NID:g28321; PIDN:CAA36422.1; PID:g28322
A;Note: part of this sequence, including the amino end of the mature protein, was con R;Sharief, F.S.; Lee, H.; Leuderman, M.M.; Lundwall, A.; Deaven, L.L.; Lee, C.; L1, S Biochem. Biophys. Res. Commun. 160, 79-86, 1989
A;Title: Human prostatic acid phosphatase: cDNA cloning, gene mapping and protein seq A;Reference number: A32419; MUID:89228054; PMID:2712834
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A;Accession: A32419
A;Molecule type: mRNA
A;Residues: 1-14,'A',16,'ASC',20,'CF',23,'C',25-94,'D',96-115,'R',117-214,'S',216-293
A;Residues: 1-14,'A',16,'ASC',20,'CF',23,'C',25-94,'D',96-115,'R',117-214,'S',216-293
A;Cross references: GB:M24902; NID:9189618; PIDN:AAA60022.1; PID:9189619
A;Note: the authors translated the codons GAC for residue 95 as Glu, CGT for residue
A;Tailor, P.G.; Govindan, M.V.; Patel, P.C.
Nucleic Roys, Govindan, M.V.; Patel, P.C.
A;Title: Nucleotide sequence of human prostatic acid phosphatase determined from a fu
A;Reference number: S11147; MUID:90370491; PMID:2395659
A;Accession: S11147
                                                                                               A;Cross-references: EMBL:X71391; NID:g416530; PIDN:CAA50514.1; R;Virkkunen, P.H.; Hedberg, P.; Palvimo, J.J.; Birr, E.; Porvar submitted to the EMBL Data Library. September 1993 A;Description: Structural organization of human and rat prostat
                                                                                                                                                                                                                                                                                                                A;Description: Characterization of the promoter of A;Reference number: S38863 A;Accession: S38863
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A;Residues: 1-14, AFASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RIWPTHPA', 74-138, 'E', 140-156
A;Cross-references: EMBL:X53605; NID:g35683; PIDN:CAA37673.1; PID:g35684
R;Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.
submitted to the EMBL Data Library, April 1993
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A;Title: Molecular cloning and sequence analysis of cDNA encoding A;Reference number: S01331; MUID:88312981; PMID:2842184

A;Accession: S01331
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A;Note: part of this sequence, including the amino end of the mature pro
R;Vihko, P; Virkkunen, P; Henttu, P.; Roiko, K.; Solin, T.; Huhtala, M
FEBS Lett. 236, 275-281, 1988
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A;Title: Structure of human prostatic acid phosphatase
A;Reference number: JH0610; MUID:92272747; PMID:1375464
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C; Species: Homo sapiens (man)
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A; Residues: 1-40 <BAN>
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A; Residues: 1-386 < VAN>
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A; Residues: 1-386 <SI
                         A; Reference number: S41251
                                                                     equence in the human gene promoter.
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F:33-386/Product: acid phosphatase ACPP #status experimental <MAT>
F:43,86/Active site: Arg #status predicted
F:44/Active site: His (phosphohistidine intermediate) #status predicted
F:94,220,333/Binding site: carbohydrate (Asn) (covalent) #status expering:161-372,215-313,347-351/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K; Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W. Biochim. Biophys. Acta 1217, 188-194, 1994
A;Title: Analysis of the promoter of the human prostatic. A;Reference number: S42730; MUID:94153995; PMID:8110833
A;Accession: S42730
                                                                                                                                                                                                         C:Accession: A61632
R:O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.
Immunol. Cell Biol. 69, 51-55, 1991
A;Title: Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stip A; Reference number: A61632; MUID:91331592; PMID:1869289
A;Accession: A61632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Snariet, F.S.; Li, S.S.

Biochem. Mol. Biol. Int. 33, 561-565, 1994

A;Title: Nucleotide sequence of human prostatic acid phosphatase ACPP gene. A;Reference number: I37175; MUID:95038536; PMID:7951074
                                                                      C; Superfamily: F; 1-17/Domain:
                                                                                                                                                                                                                                                                                                                                              granulocyte-macrophage colony-stimulating factor precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: catalyzes the hydrolysis of a wide range of phosphate esters C;Superfamily: mammallan acid phosphattase C;Keywords: 9lycoprotein; phosphohistidine; phosphoprotein; phosphoric monor;1-32/Domain: signal sequence #status predicted <SIG>
                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-144 < OAB>
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A;Map position: 3q21.3-3q25.2
A;Introns: 40/3; 72/3; 101/3; 152/3; 185/3; 216/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-386 < RES>
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A;Title: Homodimer and heterodimer subunits of human prostate acid phosphatase
A;Reference number: S17042; MUID:91336999; PMID:1908222
A;Accession: S17042
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                                                                                                                    A;Cross-references: GB:X55991; NID:g6983759; PIDN:CAA39463.1;
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C;Comment: This protein is synthesized under androgen regulation by epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                 Superfamily: granulocyte-macrophage colony-stimulating;1-17/Domain: signal sequence #status predicted <SIG>
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Similarity
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  3.2%;
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  Score 22;
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                   Length 144;
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A44936
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A;Reference number: A44936;
A;Accession: A44936
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Gene 105, 275-279,
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                                                                                                                    FQBOGM
                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-144 <NAS>
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    ;Accession:
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                                                                                                                                                                                                                                                                                                                           Local
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M.
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A;Cross references: GB:x53561; NID:g1800; PIDN:CAA37632.1; PID:g1801 C;Comment: This protein is a glycoprotein cytokine produced and secre ()Superfamily: granulocyte-macrophage colony-stimulating factor C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomum F;1-17/Domain: signal sequence #status predicted <SIG>F;18-144/Product: granulocyte-macrophage colony-stimulating factor #:
                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:S49738; NID:g233566; PIDN:AAB19466.1; PID:g233567 A;Note: sequence extracted from NCBI backbone (NCBIN:49738), NCBIP:49739) C;Superfamily: granulocyte-macrophage colony-stimulating factor F;1-17/Domain: signal sequence #status predicted <SIG>
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C;Species: Bos primigenius taurus (cati
C;Date: 31-Mar-1989 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Canis lupus familiaris (dog C; Date: 17-Feb-1994 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             granulocyte-macrophage colony-stimulating
C; Species: Canis lupus familiaris (dog)
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C;Date: 31-Mar-1992 #sequence_revision
C;Accession: JH0469; S16730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               granulocyte-macrophage colony-stimulating factor precursor -
N;Alternate names: colony-stimulating factor 2; GM-CSF
                                        N; Alternate names: colony-stimulating factor 2;
                                                           granulocyte-macrophage colony-stimulating factor
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                      (cattle)
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Pred. No.
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31-Mar-1992 #text_change
  31-Mar-1989 #text_change
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#text_change 16-Jul-1999
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Mol. Cell. Biol. 12, 883-893, 1992

A;Title: An alternatively processed mRNA from the avian c-erbB gene enco. A;Reference number: A42032; MUID:92123214; PMID:1732751

A;Accession: A42032

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-527 <FLI>
A;Cross-references: GB:M77637; NID:g211737; PIDN:AAA48759.1; PID:g211738

A;Experimental source: liver

A;Note: sequence extracted from NCBI backbone (NCBIN:76892, NCBIP:76893)

C;Superfamily: epidermal growth factor receptor; protein kinase homology

C;Keywords: ATP; growth factor receptor
                                                                    Mol. Cell. Biol. 10, 2973-2982, 1990
A;Title: A truncated, secreted form of the epidermal growth fact A;Reference number: A36325; MUID:90258888; PMID:2342466
A;Accession: A36325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-644 <PETD
A;Cross-references: GB:M37394
C;Superfamily: epidermal growth factor receptor; protein kinase C;Keywords: alternative splicing; ATP; growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermal growth factor receptor - chicken
c;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C;Accession: A42032
R;Filckinger, T.W.; Maihle, N.J.; Kung, H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Comment: This glycoprotein induces granulocyte, macrophage, and eosinophil colony C;Superfamily: granulocyte-macrophage colony-stimulating factor C;Superfamily: granulocyte-macrophage colony-stimulating factor cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell F;117/Domain: slynal sequence #status predicted <FCP F;18-143/Product: granulocyte-macrophage colony-stimulating factor #status predicted F;44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                       R;Maliszewski, C.R.; Schoenborn, M.A.; Cerretti, D.P.; Wi
Mol. Immunol. 25, 843-850, 1988
A;Title: Bovine GM-CSF: molecular cloning and biological
A;Reference number: JL0037; MUID:89096971; PMID:3062386
A;Accession: JL0037
A;Molecule type: mRNA
A;Residues: 1-143 <MAL>
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Immunol. 25, 843-850, 1988
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A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
R;Ishii, S:; Xu, Y:; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the human
A;Reference number: A25772; MUID:85270438; PMID:2991899
A;Accession: A25772
                                                                                                                                                                                                                                                                                                                                               A, Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RN A, Reference number: A00642; MUID:84245835; PMID:6330563
A; Accession: A00642; mUID:84245835; PMID:6330563
A; Molecule type: mRNA
A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-7, '99-799, 'Tp', 802-811, 'R', 813-942 <XUYY
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF re R; Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, Science 224, 843-848, 1984
A; Title: Expression cloning of human EGF receptor complementary DNA: gene amplificati A; Reference number: A43615; MUID:84196372; PMID:6326261
A; Accession: A43615
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999
C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281,
C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281,
C;Accession: A00641; A25772; S30024; A38672; Dull, T.J.; Gray, A.; Tam, A.W
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A;Residues: 1-29 <AR27
A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119;
R;Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and premature trans, Reference number: A38672; MUID:91107677; PMID:1988448
A;Accession: A38672; MUID:91107677; PMID:1988448
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A; Residues: 1-29 < HALF.
A; Residues: 1-29 < HALF.
A; Cross-references: GB: M38425; NID: g181977; PIDN: AAA63171.1; PID: g553271
A; Experimental source: carcinoma cell line A431-7
R; Xu, Y: Ishii, S: Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.;
Nature 309, 806-810, 1984
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A;Residues: 1-29 <ISH2
A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
A;Cross-reference DB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
A;Reference number: S30024; MUID:88217333; PMID:3329716
                                                                                                                                                       A; Experimental source: epidermoid carcinoma cell line A431 R; Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Ca Biochem. Biophys. Res. Commun. 124, 125-132, 1984
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A; Molecule type: mRNA
A; Residues: 1028-1210 <SIM>
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A; Residues: 713-964 <LIN>
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                                                                                 A; Accession: A23062
                                                                                                                  A; Reference number: A23062; MUID: 85046483; PMID: 6093780
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s: protein-tyrosine kinase (EC 2.7.1
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Speiss,

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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: A53183; A43818; S249442; A28941; S45325; I49643
R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jer Genes Dev. 8, 399-413, 1994
A;Title: The mouse waved-2 phenotype results from a point mutation in the E(A;Reference number: A53183; MUID:94170986; PMID:8125255
A;Accession: A53183
A;Title: Comparison of EGF receptor sequences as a guide A;Reference number: A43818; MUID:91232866; PMID:2030916 A;Accession: A43818
                                                                                                                         A:Cross-references: GB:U03425
R;Avivi, A.; Lax, I.; Ullrich,
Oncogene 6, 673-676, 1991
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F;718-726/Region: protein kinase ATP-binding motif
F;999-1046/Region: coated-pit mediated internalization signal
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A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.;
Cell 59, 33-43, 1989
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A;Residues: 25-30,'S',32-51;454-467 <WEB>
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros,
J. Biol. Chem. 260, 5205-5208, 1985
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A; Residues: 1-1210 <LUE>
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A; Residues: 740-744, 'X', 746-747 < RUS>
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Keywords: ATP; autophosphorylation; duplication; glycoprotein; phospho
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0-273, 1984
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RESULT 14
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A; Molecule type: protein
A; Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-10
R; Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A; Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Recept
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J. Biol. Chem. 263, 13152-13158,
A;Title: Epidermal growth factor
                                                                                                                                                                                                                                                                                      epidermal growth factor receptor precursor - chicken N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Gallus gallus (chicken) C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
A;Cross-references: GB:M20386 R;Nilsen, T.W.; Maroney, P.A.;
                                                         A; Molecule type: mRNA
A; Residues: 1-1223 <LAX>
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A; Residues: 12-20,22-132 <RES>
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A; Residues: 969-971, 'K', 973-1115, 'D'
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                                                                                                                                              A;Title: Chicken epidermal growth factor (EGF) receptor: A;Reference number: A27720; MUID:88261272; PMID:3260329
                                                                                                                                                                                                    R;Lax, I.; Johnson, A.; Howk, R.;
Mol. Cell. Biol. 8, 1970-1978, 191
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A; Residues: 1-971, 'K', 973-1210 <VER>
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A;Accession: A28941
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;712-977/Domain: protein kinase ATP-binding motif
;720-728/Region: protein kinase ATP-binding motif
;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimenta
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:1197/Binding site: phosphate (Tyr) (covalent) #status experimental
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263, 13152-13158, 1988
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Best Local Similarity
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F;727-735/Region: protein kinase ATP-binding motif
F;127-735/Region: protein kinase ATP-binding motif
F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (F;192,650/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;754/Active site: Lys #status predicted
F;754/Active site: hosphate (Tyr) (covalent) (by autophosphorylation) #stat
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A;Accession: A00643
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R;Smith, L.R.; Lundeen, K.A.; Diveley, J.P.; Carlo, D.J.; Brostoff, S.W. Immunogenetics 39, 80, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         granulocyte-macrophage colony stimulating factor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Jul-1999
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Search completed: April 28, 2003, 13:46:15 Job time : 26 secs
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                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-127 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: I46269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Nucleotide sequence of the Lewis rat granulocyte-macrophage colony stimulating A; Reference number: I46269; MUID:94041474; PMID:8225444
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A; Residues: 585-1223 <NIL>
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31-654/Domain: extracellular #status predicted <EXT>
81-307/Domain: EGF receptor extracellular domain repeat <EE1>
397-610/Domain: EGF receptor extracellular domain repeat <EE2>
655-677/Domain: transmembrane #status predicted <TMM>
678-1223/Domain: intracellular #status predicted <INT>
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nes 8; Conserv
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0; Mismatches
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Maximum DB seq length: 200000000
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Match
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Gapop 60.0 , Gapext 60.0
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000, DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000, DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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                                       Human HER500-hGM-C
Human HER500 fusio
Human HER500 fusio
Human HER500-rGM-C
Human HER500-rGM-C
Human ErbB2 oncopr
Human ErbB2 extrac
Extracellular HER-
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HER-2/neu fu
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23	23	21	14	22	22	19	22	20	19	22	22	22	23	21	22	23	23	23	23	23	22	22	22	22	21	21	21	20	17	21	23	21	18	23
AAE20483	AAM51146	AAB21201	AAR39568	AAB48763	AAB62074	AAW59345	AAB48767	AAY14572	AAW59354	AAE13123	AAE13122	AAE13121	AAU98923	AAY44993	AAE13120	AAU74545	AAU77114	AAM51143	AAE20479	AAE24067	AAB60167	AAG88267	AAB85458	AAE12130	AAY92620	AAY84780	AAB21198	AAW92406	AAW01111	AAB21208	ᇤ	AAB21203	976	AAM51149
 Human protein for	Human Her-2/neu on	HER-2/	Sequence of c-erbB	Human ErbB2 extrac	ErbB2 protein doma	Human ErbB2 domain	Human ErbB2 N-term	Human erbB2 recept	ρrg	ART3-IC-F		e human HER-	2	v-erbB2EC f	e huma	HER2 (ErbB2	Her-	Her-2/neu	Her-2/	Human Her-2 prote1	transgene	neu amino a	Human HER-2/neu pr	tyrosine k	hereg	acid seque		Human HER-2/neu on	/neu prote	HER-	extrac	`	-GM-CS	Her·2/neu extracel

ALIGNMENTS

XX PA (DEND-) DENDREON CORP. XX	XX PR 30-MAR-2000; 2000US-193504P.	XX PF 30-MAR-2001; 2001WO-US10515.	PD 11-0CT-2001.	PN WO200174855-A2.	XX	Chimeric	OS Chimeric - Homo sapiens.					KW dendritic cell; o		KW Immunostimulatory		28-JAN-2002	XX	AC AAE13109;	XX	AAE13109 ID AAE13109 standard	RESULT 1
CORP.)US-193504P.	LWO-US10515.				etic.	apiens.	HER500-hGM-CSF fusion protein.	anulocyte-macrophage colony stimulating factor;	membrane distal intracellular domain; C-terminal tag; human; GM-CSF;	PAP protein; Ala Arg linker; membrane distal extracellular domain;	dendritic cell; colon cancer; breast carcinoma; ovarian cancer;	immunostimulatory component; T-cell mediated immune response; DC;	Immunostimulatory fusion protein; IFP; antigen component; therapy;	Human HER500-hGM-CSF fusion protein construct.	(first entry)		•		109 AAE13109 standard; Protein; 690 AA.	

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WPI; 200
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HER-2 a
                           2001-662965/76.
DB; AAD21565.
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immunostimulatory fusion protein comprising the intracellular domain HER-2 and an antigen elicits an immune response to the antigen and useful for the treatment of associated cancer associated -

Claim 7; Page 26; 59pp; English.

immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 hGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains, an Ala Ala linker, a mature human granulocyte-macrophage colony stimulating factor (GM-CSF) sequence and a The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC) induced T-cell mediated cellular tag.

Sequence 690 8

Query Best L

Local

Similarity

100.0%;

Score 690; Pred. No. 0;

DB

Length

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Match

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Matches
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                                                                                   MPNPEGRYTFGASCVTACPYNYLSTDVGSGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
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                                                                                                                                                                                    EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
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MRAAPLLLARAASLSLGFLFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPET

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               nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 fusion protein construct which comprises human pAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains and a C-terminal tag.
 Sequence
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Chimeric -
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                                                                                                                                                                                                     Claim 7; Page 26; 59pp; English.
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Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human HER300-rGM-CSF fusion construct comprising OVA-derived peptide.
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Matches 329;
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                                                   Chimeric - Homo sapiens.
Chimeric - Unidentified.
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                                                                                                          dendritic cell; colon cancer; breast carcinoma; ovarian cancer; 
PAP protein; Ala Arg linker; membrane distal extracellular domain; 
membrane distal intracellular domain; C-terminal tag; human; OVA; 
HER-2 protein; ovalbumin-derived octapeptide; HER500 fusion protein
                                                                                                                                                                                                                                      Human HER500
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immunostimulatory component; T-cell mediated immune response; DC;
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                                                                                                        protein; ovalbumin-derived octapeptide;
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                                                                                                        fusion protein
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WO200174855-A2

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RESULT 5
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   Human HER500-rGM-CSF
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                                                                                                    AAE13111 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 26; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulatory fusion protein comprising the intracellular domain HER-2 and an antigen elicits an immune response to the antigen and useful for the treatment of associated cancer associated -
                                                                                                                                                                                                     MPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                                                                                                                                                                                                                                                   GGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
                                                                                                                                                                                                                                                                                                                                    CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
                                                                                                                                                                                                                                                                                                                                                                                                   VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI
                                                                                                                                                                                                                                                                                                                    CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
                                                                                                                                                                                                                                                                                                                                                                                VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL
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                                                                                                                                                                                                                                                     GGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
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                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               distal intracellular domain and a C-terminal tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.78;
 fusion
construct comprising OVA-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 329; DB 22;
Pred. No. 3.9e-293;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 564;
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В Ş

181

181 121

CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA

240

GGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA

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121

61

61 HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI 120

MRAAPLLLARAASLSLGFLFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPET

60

0

HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI 120

VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL

180 180

VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGCVLIQRNPQL

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Matches
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Best Local
                                                                                                                                                            The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 rGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal intracellular domain, an Ala Ala linker, a mature PAP and a granulocyte-macrophage colony stimulating factor (GM-CSF) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - 1
Chimeric - 1
Chimeric - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF; HER-2 protein; granulocyte-macrophage colony stimulating factor; ovalbumin-derived octapeptide; OVA; rat; HER500-rGM-CSF fusion prote
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US10515
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 27; 59pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          is useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunostimulatory fusion protein;
1 MRAAPLLLARAASLSLGFLFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunostimulatory fusion protein comprising the intracellular domain HER-2 and an antigen elicits an immune response to the antigen and useful for the treatment of associated cancer associated -
                                                                                                                                                  granulocyte-macrophage
a C-terminal tag.
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DB; AAD21567.
                                                   329;
                                                                 Similarity
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Rattus norvegicus.
Unidentified.
                                                                                                                  697 AA;
                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                               47.78;
                                               0
                                                                 Score 329; DB 22; pred. No. 4.6e-293;
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                                                 Mismatches
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                                                                               Length
                                               Indels
                                                                                 697;
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Best Local Similarity

100.0%;

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RESULT 6
AAB60408
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                                          CC comprising administering an antibody which binds Errb2 (HER2; AAB60408).

CC In particular, the anti-Errb2 antibody is the murine monoclonal antibody CC 224 (AAB60396, AAB60397) or a humanised version of 224 (AAB60398.

CC AAB60399). The invention also encompasses an isolated nucleic acid CC encoding a humanised ErbB2-binding antibody; vectors and host cells CC comprising such nucleic acids; the recombinant production of a humanised CC ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies CC act by antagonising ErbB receptors, and as inhibitors of transforming CC growth factor alpha (TGF-alpha)-activated mitogen activated protein CC kinase (MAPK). The method of the invention is used for treating cancer, CC especially colon cancer, rectal cancer, colorectal cancer (especially colon cancer, rectal cancer), or breast cancer (especially CC uses e.g., as affinity purification agents. Using an antibody which binds to ErbB2 to treat cancer is preferable to the use of EGFR-targetted CC drugs, as EGFR is also highly expressed in other tissues such as the CC liver and skin, where the active drugs. Antibodies which bind CC ErbB2 are anticipated to have a better safety profile than such drugs.

CC The present section of the profile than such drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  light chain variable region; cancer; cytostatic; EGFR-exprepidermal growth factor receptor; colon cancer; rectal carcolorectal cancer; non-small cell lung cancer; metastatic
                                                                                                                                                                                                                                                                                                                                                                                                                               wherein the cancer expresses epidermal growth factor receptor (EGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for treating cancer in a human patient,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating cancer in a human, where the cancer expresses epidermal growth factor receptor (EGFR), comprises administering an antibody which binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-ErbB2 monoclonal antibody 2C4; HER2; mouse; light chain variable region; cancer; cytostatic;
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                                   present sequence represents
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645
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                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; HER2; mouse; murine; humanised; VI; crytostatic; EGFR-expressing cancer colon cancer; rectal cancer; tumour lung cancer; metastatic breast cancer
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                                     ErbB2.
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tumour;
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Score

292;

DB 22;

Length

Query Match

Score

292;

DB 22;

Length

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RESULT 7
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                                       The ErbB family of receptor tyrosine kinases are important mediators of cell growth, differentiation and survival. The receptor family includes four distinct members including Epidermal Growth Factor Receptor (EGFR of ErbB1), HER2 (ErbB2 or pl85°neu), HER3 (ErbB3) and Her4 (ErbB4 or tyro2). The present invention relates to a method for treating prostate cancer. The method comprises administering an antibody which binds ErbB2 and blocks ligand activation of an ErbB receptor. Preferably, the antibody blocks binding of monoclonal antibody 2C4 to ErbB3 and/or blocks. The method comprises and/or blocks in the interpretation of mitogen-activated protein kinase (MAPK). The
                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                        Agus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ErbB2; antibody; ErbB
Sequence
                                                                                                                                                                                    Disclosure; Fig 1; 93pp; English
                                                                                                                                                                                                                                 Treating
                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-2001
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                            present sequence is
                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLS&LQDIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ
                                                                                                                                                                                                                                                                                        DB,
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                                                                                                                                                                                                                 ing prostate cancer in a human comprises administering an antibody binds ErbB2 and blocks ligand activation of an ErbB receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ErbB2
                                                                                                                                                                                                                                                                                        Scher HI,
 645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       extracellular
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                                                                                                                                                                                                                                                                                          Sliwkowski MX
                            extracellular domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoclonal antibody 2C4; variable 11
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; Mismatches 0;
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Matches
                                                                                                       The present sequence is the extracellular HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGRR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or companion of the protein companion.
                                                                                                                                                                                                                                                                                                                                                  HER-2/neu extracellular domain/phosphorylation domain useful for vaccinating against breast, ovarian, colon, prostate cancers -
                                           to treat malignancies such prostate cancers, and may k
                                                                                                                                                                                                                                                                                                  Claim 2; Fig 9; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheever MA,
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                                                                                           enhancing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-1999;
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SMITHKLINE BEECHAM
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92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gheysen
                                                              immune response to the HER-2/neu protein. It may ignancies such as breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                             to vaccinate
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                                                                                      It may be used
                                                                                                                                                                                                                                                                                                                                                                       Lung
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Best Local
                                                                                                                            Her-2/neu fusion protein for treating or preventing ce
or enhancing an immune response to the protein, has He
extracellular domain fused to Her-2/neu intracellular
                                                                                                Claim 2;
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                                                                                                                    phosphorylation domain
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                                                                                                                                                                                      Cheever MA,
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292; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Her-2/neu oncoprotein
                                                                                                                                                                                                          CORIXA CORP
                                                                                               F1g 9;
                                                                                                                                                                                                                                                                                                                                      kinase;
                                                                                                                                                                                                                                                                                                                                              oncogene;
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                                                                                               141pp; English.
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                                                                                                                                                                                                                                                                                                                                               tumour; vaccine; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 292; DB 21;
Pred. No. 4.1e-259;
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                                                                                                                                      cancer by
Her-2/neu
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The present sequence is that of the extracellular domain of human Her-2/neu (p185 glycoprotein or c-erb82), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu (see AAM51143) is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain of munne phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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(CORI-) CORIXA CORP.
(SMIK ) SMITHKLINE BEECHAM
                                          29-JAN-1999;
                                                                     28-JAN-2000;
                                                                                                                             WO200044899-A1
                                                                                                                                                         Synthetic
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                              Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
breast cancer; prostate cancer; ovarian cancer; lung cancer;
                                                                                                                                                                                                                                                        Human HER-2/neu fusion protein
                                                                                                                                                                                                                                                                                     12-JAN-2001
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Similarity 100.0%;
92; Conservative (
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RESULT 11
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                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                       Her-2/neu extracellular domain-delta-phosphorylation domain
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                                                                       /note= "extracellular 654..712
                                                                                                                 Location/Qualifiers
                                                                                                                                                                            receptor;
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eptor; c-erbB2; ;
                                                       "phosphorylation domain fragment"
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Pred' No. 4.4e-259;
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WO200212341-A2

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The invention provides Her-Z/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of Her-Z/neu is fused to a Her-Z/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune response to Her-Z/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a specific T-cells are useful for inhibiting the development of a
AAW19764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of a fusion protein between the extracellular domain and a fragment (DeltaPD) of the phosphorylation domain of human Her-2/neu (see AAM51143), an oncogenic self-protein and target for anti-cancer vaccines. The fusion protein can be obtained by recombinant DNA methods. Her-2/neu overexpression
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                            AAW19764 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Pred. No. 4.4e-259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potent APC that activates T-cells to immune response - can also induce a c vertebrate subject
                                                                                                                                                                                                                                                                                          Sequence
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growth factor
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                           CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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                                                                                                                                                                                                                                                                                          782 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 8; 45pp; English.
                                                                                                                                                                                                                                Conservative
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r receptor; oncogene; immunostimulant; cancer; ~
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Pred. No. 4.7e-259
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a fusion protein comprising the extracellular domain and the phosphorylation domain of the human HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. They may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against these neoplasias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; breast cancer; prostate cancer; ovarian cancer; lung cancer; colon cancer; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HER-2/neu extracellular domain/phosphorylation domain fusion useful for vaccinating against breast, ovarian, colon, lung
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                                                                                                   ELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPM
                                                                                                                                                                                                                      GAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQ
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SMITHKLINE BEECHAM
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response to Her-Zyneu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. To cells that specifically react with a Her-Zyneu fusion protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                                                                The present sequence is that of a fusion protein between the extracellular domain and phosphorylation domain of human Her-2/neu (see AAM51143), an oncogenic self-protein and target for anti-cancer vaccines. The fusion protein can be obtained by recombinant DNA methods. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu tusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain or her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its Deltapp fragment). An immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain
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Query Match Best Local

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           The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation
                                                                                                                     HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and prostate cancers -
                                                                                                                                                                                                                               (CORI-)
   domain
                                                                                               Disclosure; Fig 15; 128pp; English.
                                                                                                                                                                      WPI; 2000-505976/45.
N-PSDB; AAA89736.
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                    NHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329
                                          CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF
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Search completed: April 28, 2003, 13:44:37 Job time: 43 secs

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-OB--Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -NATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALION-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-USO9821883_@CGN_1_1 80_@runat_28042003_104750_14608
-NCPU-6 -CTCPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDF-10 -XGAPEXT-0.5 -FGAPDP-6
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:/cgn2_6/ptodata/1/pubpna/US08.NEW_FUB.seq:*
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:/cgn2_6/ptodata/1/pubpna/US09.PUBCOMB.seq:*
:/cgn2_6/ptodata/1/pubpna/US10_NEW_FUB.seq:*
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                                                                              CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 2070
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-821-883-7
           Alignment Scores
Pred. No.:
                                                 US-09-821-883-7
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APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Demir
APPLICANT: Vidovic, Demir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09821883 Patent No. US20020061310A1
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Length: Matches:

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110 US-09-811-115-2
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110 US-09-854-356-11
110 US-09-851-883-24
110 US-09-851-883-24
110 US-09-930-125-6
110 US-09-930-125-6
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110 US-09-930-13-1-1
110 US-09-940-101-1
1110 US-09-940-101-3
1110 US-09-940-3
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Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli Sequence 8, Appli Sequence 8, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 24, Appli Sequence 28, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 165, Appli Sequence 165, Appli Sequence 1731, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 300, Appli

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681 ProAlaAlaAlaHiSHiSHiSHiSHiSHiS 690	Оу	21 AsnTy	Qy V
661 PheLeuLeuVallleProPheAspCysTrpGluProValGlnGluGlyAlaProProPr 	Оу	etProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysProTyr 32 	ş Ş
641 1921	Оу		Oy Oy
621 LeuLysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrPro	Qγ	m N	Db Oy
601 ThrcysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLys	Оу	7 2	Оy
581 AlaAlaGluMetAsnGluThrValGluValIleSerGluMetPhaAspLeuGlnGluPro	Оу	221 SerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCysAla 240	Оу
561 1681	Db	201 ThrLeulleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGly 220 	Db Oy
1621	рр	181 CysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeu 200 	Qy db
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1441	Db Oy	121 ValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAsp 140 	Оy
1381 2	Db Cy	101 GlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArgIle 120 	ob oy
1321		81 LeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGln 100 	Оy
1261		61 HisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeuGlu 80 	Qy Db
1201	ob Cy	41 SerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThr 60 	p oy
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APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT FAPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR PILING DATE: 2000-03-30
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SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: LAUS, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Der
TITLE OF INVENTION INVENTIONS US/09/821,883
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 1665
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                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial
FEATURE:
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                                    AspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSerLeuProThrHisAspProSerPro
                                                                       GluAlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGly
                                                                                                                   MetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysProTyr
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APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEO for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity:
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ORGANISM: Artificial Sequence
FEATURE:
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TOTAL TO
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	391.	372 GlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGln	Qy
	1140	081 ACACTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCG	Db 1
	371	352 ThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGlu	Qy
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	1020	21 ASTIYLEGUSETTIKASPYGLSTYSEET	
	் க்	01 ATGCCCAATCCCGAGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGTCCTA	Db
	320	01 MetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCy	
٠.	900	281 GlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSer	Оy
	84 Q.	781 GCGGGCTGCACGGGCCCCAAGCACTCTGACTGCCTGGCCTGCCT	
	280	61 AlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHisS	
	780		•
	260	41 GlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCysA	
	720	221 SerargCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCysAla	Qy Db
	6	01 ACACTGATAGACACCAACCGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAA	•
	220	201 ThrLeuILeAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGly	Qy
	600	541 TGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCTCTC	·
	200	81 CysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLe	Qy
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	180	.61 LeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGlnLe	
	8	421 CCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCCAGGAGGCCTGCGGGAGGCTGCAGAG	
	D.	1 ProlenasnasnThrThrProValThrGlvAlaSerProGlvGlvIlenargGlnLenG	
	140 420	121 ValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAsp 	Ωy
	360	01 GCTACGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGCC	DЪ
	120	AlaHisAsnGlnValArgGl	
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	60	${\tt rThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThr}$	Qy

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT: MONAHAN, JOHN J.
APPLICANT: HANGTON, BEATRICE CLAUDIA
APPLICANT: HANGOCK, MIRIAM E.C.
APPLICANT: BLUFORD, PETER
TIPLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
FILE REFERENCE: BEBIO-111-C1
CURRENT APPLICATION NUMBER: US/09/769,508
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (150)..(3914)
US-09-769-508-1
                       US-09-821-883-2 (1-690) x US-09-769-508-1 (1-4543)
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                                                                                                                                                                               LENGTH: 4543
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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2 ArgAlaAlaProLeuLeuAlaArgAlaAlaSerLeuSerLeuGlyPhe------
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                                             Conservative: Mismatches: Indels: Gaps:
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Matches:
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329		329	Qy
1133	GEATCCTGCACCCTCGTCTGCCCCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACA	1074	뮹
329	lySer	328	Qy
1073	TATACATTCGGCGCCAGCTGTGTGACTGCCTGTCCCTACCACCTTCTACGGACGTG	1014	В
327	yrThrPheGlyAlaSerCysValThrAlaCysProTyrAsnTyrLeuSerThrAspVal	308	οy
1013	PTOALBURGITATIYYASITTATASPYTATPHEGIUSETMECPTOASHPYOGIUGIYATG	954	B 2
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287	HisSerAspCysLeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLeuHisCys HisSerGlyIleCysLeuHisPheAsnHisSerGlyIleCysGluLeuHisCys HisSerGlyIleCysGlu	268	3 5
893	GGCCACTGCCCACTGACTGCCATGAGCAGTGTGCTGCCGGCTGCACGGGCCCCAAG	834	рь
267	roLeuProThrAspCysCysHisGluGlnCysAlaAlaGlyCysThrGlyProLys	248	Qγ
ώ.		7	Db :
-	erGluAspCvsGlnSerLeuThrArgThrValCvsAlaGlvGlvCvsAlaArgCvsLvs	N	o V
773	TCTCGGGCCTGCCACCCTGTTCTCCGATGTGTAAGGGCTCCCGCTGCTGGGGAGAGAGA	714	B 5
, ,	GGAAGGACATCTTCCACAAGAACCAACCGC	י כ)
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653	TGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAGCTCTGCTACCAGGACACGATTTTG	594	В
187	LeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeuCysTyrGlnAspThrIleLeu	168	Q
593	ი-	534	Дb
167	alThrGlyAlaSerProGlyGlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIle	148	Qy
533	GAGGACAACTATGCCCTGGCCGTGCTAGACAATGGAGACCCGCTGAACAATACCACCCCT	474	Db
147	luAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAspProLeuAsnAsnThrThrPro	128	Qy
473	AACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGCGGATTGTGCGAGGCACCCAGCTCTTT	414	Вb
127	snGlnValArgGlnValProLeuGlnArgLeuArgIleValArgGlyThrGlnLeuPhe	108	Qy
413	GCCAGCCTGTCCTTCCTGCAGGATATCCAGGAGGTGCAGGGCTACGTGCTCATCGCTCAC	354	рь
107	laSerLeuSerPheLeuGlnAspIleGlnGluValGlnGlyTyrValLeuIleAlaHis	88	Qy
353	CTCTACCAGGGCTGCCAGGTGGTGCAGGGAAACCTGGAACTCACCTACCT	294	В
87	euTyrGlnGlyCysGlnValValGlnGlyAsnLeuGluLeuThrTyrLeuProThrAsn	68	ОУ
293	ACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAGACCCCAGCTGGACATGCTCCGCCAC	234	рь
67	hraspMetLysLeuArgLeuProAlaSerProGluThrHisLeuAspMetLeuArgH	48	Qy
233	GGGCTCCTCGCCCTCTTGCCCCCCGGAGCCGCGAGCACCCAAGTGTGCACCGGC	177	Б
47	alLeuAlaLysGluLeuAlaArgGlyAlaAlaSerThrGlnValCysThrGl	28	Qy
176	AGCCGCAGTGAGCACCATGGAGCTGGCGGCCTTGTGCCGCTGG	123	₽
27	LeuPheLeuLeuPhePheT	19	οy
122		63	Db

	AGACTGCTGCAGGAAACGGAGCTGGTGGAGCCCGCTGACACCTAGCGGAGCGAACCAAC 2273	GTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATCCGGGAAGTACACGATGCGG 2213	WARFILLIAMESTERMINGTERMESTAGETAGETERMINESTERMINGTERMINESTERMINGTERMINESTERMINGTORMING			AACTGCACCCACTCCTGTGTGGACCTGGATGACAAGGGCTGCCCCGCCGAGGAGAGAGA		TCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATC 2033		CACTATAAGGACCCTCCCTTCTGCGTGGCCCGCTGCCCCAGCGGTGTGAAACCTGACCTC 1973		TO COAGAATOROTO ACTRATOTO TOTO TOTO ACCORACION TOTO ACTRATOTO ACTR		・ 28 1 - 94 04504のようしゅく こうじゅうしょうしゅうしゅうじゅうしゅうじゅうじゅうじゅうじゅうじゅうじゅうじゅうじゅうじゅうじゅうじゅうじゅうじゅ		GTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGCGTGGAGGAATGCCGAGTACTGCAG 1793		CTGGCCTGCCAGCTGTGCGCCCGCAGGGCACTGCTGGGGTCAGGGCCCACCCA		CCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCAGAGGACGAGTGTGTGGGGGGAGGGC 1673		CACCATAACACCCACCTCTGCTTCGTGCACACGGTGCCCTTGGGACCAGCTCTTTTCGGAAC 1613		3.2.5 1. DAY DESCRIBERTANDES DE SERVICE DE SERVICE DE SELLA CELLA CELLA CELLA CELLA CELLA CELLA CELLA CELLA CELLA CE	CANDIANICUSUSANDANITUTUS CANAISUS CONTROLICOS TRACECTOS CANAISES (18 1493		INCELETATION TO THE TRANSPORT TO THE TOTAL TO THE TOTAL TOTA					AAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGCTTTGATGGGGACCCAGCCTCCAAC 1313			
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	341 SerSerSerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSerGluGlu 360	3234 GGCTTCTTCTGTCCAGACCCTGCCCCGGGGGCCTGGGGCATGGTCCACCACAGGCACCGC 3293		3174 CTGGAGGACGATGACATGGGGGGACCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAG 3233	329 329	3114 ATCCAGAATGAGGACTTGGGCCCAGCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTG 3173	329 329	3054 TTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCCAGGGACCCCCAGCGCTTTGTGGTC 3113	329 329	2994 ATTGATGTCTACATGATCATGGTCAAATGTTGGATGATTGACTCTGAATGTCGGCCCAAGA 3053	329 329	2934 CGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGGCTGCCCCAGCCCCCATCTGTACC 2993	329 329	2874 GGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCCCAAACCTTACGATGGGATCCCAGCC 2933	329 329	2814 ATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACCCACC	329 329	2754 CTGCTGGACATTGACGAGACAGAGTACCATGCAGATGGGGGCCAAGGTGCCCATCAAGTGG 2813	329 329	2694 CGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAAATTACAGACTTCGGGCTGGCT	329 329	2634 ATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGGCTCGTACACAGGGACTTGGCCGCT 2693	329 329	2574 CATGTCCGGGAAAACCGCGGGACGCCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAG 2633	329 329	2514 TGCCTGACATCCACGGTGCAGCTGGTGACACAGCTTATGCCCTATGGCTGCCTCTTAGAC 2573	329 329	2454 GACGAAGCATACGTGATGGCTGGGGTGTGGGCTCCCCATATGTCTCCCCGCCTTCTGGGCCATC 2513	329 329	2394 CCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCCCCCAAAGCCAACAAAGAAATCTTA 2453	329 329	2334 GGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATCCCTGATGGGGGAGAATGTGAAAATT 2393	329 329		2274 CAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCT 2333

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; LENGTH: 4530
; TYPE: DNA
; ORGANISM: HOMO :
US-09-877-177-11
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                                                            Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                         Sequence 11, Application US/09877177 Publication No. US20020192652A1 GENERAL INFORMATION:
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                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/877,177
CURRENT FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                        APPLICANT: Peter V. Danenberg et al.
TITLE OF INVENTION: Method of determining
TITLE OF INVENTION: Factor Receptor and H
FILE REFERENCE: 11220/120
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371 GluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 390		CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG
351 LeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer 370	Qy Db	
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3145 CCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTG 3204	Db	GACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTGTGCGGTG
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329 329	VQ	CUCTUCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCCATCTGGAAAGTTTCCAGAT
3025 TGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGGAGTTGGTGTCTGAATTCTCCCGC 3084	Db.	
329 329	γo	1000 CUGGAGGCTGACCAGTGTGTGCCTGTGCCCCACTATAAGGACCCTCCCT
2965 GAGCGGCTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT 3024	Db	
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2665 GTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAT 2724	. dd	ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC
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2605 TCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGAT 2664	Db	1525 AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 1584
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2485 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA 2544	Db	CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAAT
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2425 ACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC 2484	da .	GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC
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2365 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2424	מם	1285 GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG
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APPLICANT: Sharon Erickson
APPLICANT: Mark Silwkowsil
APPLICANT: Mark SILWkowsil
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENERT 073A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                               : ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Vector Sequence
US-09-811-123-7
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LENGTH: 9274
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2756	ACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGAGTGTGC	Db 2697	
329		Оу 329	
2696	TyrLeuSerThrAspValG1ySer	Oy 322 Db 2637	
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2576 301	ATCTGTGAGCTGCACTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGAGTCCATG	251	
301	IleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMet	Оу 282	
281 2516	2 GlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHisSerGly	Qy 263 Db 2457	
261 2456	() — 10	Qy 247 Db 2397	
	CGCTGCTGGGGAGAGTTCTGAGGATTGTCAGAGCCTGACGCGCACTGTCTGT	233	
2336	AGACACCAACCGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAQGGCTCC STroGlvGluSerSerGluAspCvsGloSerIeuThrArgThrVallvsAlaGlv	227	
21	2 LeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGlySer	20	
201 2276	TyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeuThr	Qy 182 Db 2217	
181	2 ArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAanProGlnLeuCys	Oy 163	
1 6	\ThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeuGlnLeu 	4 0	
141 2096	ArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAspPro 	Qy 122 Db 2037	
0	2 TyrValLeuIleAlaH1sAsnGlnValArgGlnValProLeuGlnArgLeuArgIleVal	Oy 103 Db 1977	
101 1976	2 ThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGly	Oy 8:	
81 1916	euGluLeu TGGAACTC	Oy 63	
61 1856	2 ThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThrHis	Qy 4: Db 1797	
41 1796	LeuPhePheTrpLeuAspArgSerValLeuAlaLysGluLeuAlaArgGlyAlaAlaSer 	Оу 22 Db 1746	··· -
1745	2 AIGAIAALARIOLEULEULEULEULAITGAIGAGCCGGAGCCATGGAGCTGGCGGCC :	Db 1699	

3777 CGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGACCGCTGACACCT 3836 329 329	329 329	3717 CTGGTCGTGGTCTTGGGGGTCTTTGGGATCCTCATCAAGCGACGGCAGAAGATC 3776		3657 CCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGCATTCTG 3716	329 329	3597 TGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGATGACAAGGGCTGC 3656	329 329	3537 GGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTTCCAGATGAGGAGGGCGCA 3596	329 329	3477 CAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCTTCTGCGTGGCCCGCTGCCCCAGC 3536	329 329	TGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAGGCTGAC		GAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGTTTGCCG		CCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGCGTGGAG		3237 GAGTGTGTGGGGGGGGGCCTGGCCACCAGCTGTGCGCCCGAGGGCACTGCTGGGGT 3296	329 329	GACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCAGAGGAC	311/ ASTESACTISSCUTCATUACIATIAACACUCACCTUTSCTTUSTSCACAGGGGCCCTGS 31/8		רי אטעררר ז מרעעמממר ז מממרטז רעמר ז ממר ז מממר ז מרטר ז רער ז מרשממטער ז מממר		ABLBTCTTCCABANCCTGCAABTAATCCGGGGACGAATTCTGCACAATGGCGCCCTACTCG		**************************************	つまつしゅうじょうしゅ しゅうじょうじゅうしゅうじゅうじゅうしゅ しゅうしゅじゅうじゅう とうしゅうじゅう アンドラン・アントランド しゅうしゅう		GGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTTTGAGACT	329 329	2817 GAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTTGGCATTTCTGCCGGAGAGCCTTTGAT 2876	329 329	2757 TATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGTGCCAATATCCAG 2816	329 329
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355 LeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGlyAlaGly	33 ValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThrLeuGly 354	4797 TATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGGGGGCACC	330GlyAlaGlyGlyMet 334	4737 ACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCTGAGGAG 4796		4677 CCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	329	4617 TCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCCAGGGAC	329	455/ CAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATGATTGAC	3.29	4497 TACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGGCTGCCC	329 329	4437 AGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTTGGGGCCCAAACCT 4496	329 329	4377 AAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACCCACC	329 329	4317 GACTTCGGGCTGGCTGGCTGGACATTGACGAGACAGAGTACCATGCAGATGGGGGC 4376		4257 CACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAAATTACA 4316	329 329	4197 CTGAACTGGTGTATGCAGATTGCCAAGGGGGATGAGCTACCTGGAGGATGTGCGGCTCGTA 4256	329 329	4137 TATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGCTCCCCAGGACCTG 4196	329 329	4077 TCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTTATGCCC 4136	329 329	4017 GCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCATATGTC 4076	329 329	3957 GGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCCCCCAAA 4016	329	GTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATCCCTGAT		HAPPAHAPPAHAPPAHAPPAHAPPAHAPPAHAPPAHAP	2000

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	; OTHER INFORMATION: Vector Sequence US-09-811-115-1	: LENGTH: 9274 : TYPE: DNA : ORGANISM: Artificial Sequence : FEATURE:	PRIOR FILING DATE: 2000-03-16 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0	FILE REFERENCE: GENENT.034A CURRENT APPLICATION NUMBER: US/09/811,115 CURRENT FILING DATE: 2001-03-16 PRIOR APPLICATION NUMBER: 60/189,844	APPLICANT: Erickson, Sharon ; APPLICANT: Schwall, Ralph ; APPLICANT: King, Kathleen ; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL	RESULT 8 US-09-811-115-1 Sequence 1, Application US/09811115 ; Patent No. US20020035736A1 ; GENERAL INFORMATION:	Oy 575 AsnLeuSerArgAspThr 580 ::: ::: Db 5562 AGCTATTCCAGAAGTAGT 5579		5457 GCAGAGCACCCAGAGTACCTGGGTCTGGACGTGCCAGTGTGAACCCAGAAGGCCA 5457 SerProSerThrGlnProTrnGlnHigValagnalaileGlnGlnAlaargargienien	5397	5337 GCTGCCCCTCAGCCCACCCTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTAC	5277 GACGTTTTTGCCTTTGGGGGTGCCGTGGAGAACCCCGAGTACTTGACACCCCAGGGAGGA	11111111111111111111111111111111111111	11			Qy 395 ThrHisaspproSerProLeuGlnArgTyrSerGluAspproThrValProLeuProSer 414	375 SerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLySGlyLeuGlnSerLeuPro	Db 4917 CTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGGGCTGGC 4976
Qy	Оу	Оу	Qy	Оу	Qy	Qγ	Оу	Оу	Qy dd	Qy	. Qy	Оу	QY	Qy	Qy	Оу	. US	Bes Que DB:	Pe
322 TyrLeuSerThrAspValGlySer 329	302 ProasnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysProTyrAsn 321 	282 IleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMet 301 	262 GlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHisSerGly 281	242 GlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCysAlaAla 261 	222 ArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCysAlaGly 241	202 LeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGlySer 	182 2217	162 ArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeuCys 181	142 LeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeuGlnLeu 161 	122 ArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAspPro 141	102 TyrvalleulleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArgTleVal 121	82 ThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGly 101	62 LeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeuGluLeu 81 	42 ThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThrHis 61 	22 LeuPhePheTrpLeuAspArgSerValLeuAlaLysGluLeuAlaArgGlyAlaAlaSer 41	2 ArgAlaAlaProLeuLeuAlaArgAlaAlaSerLeuSerLeuGlyPheLeuPheLeu 21	US-09-821-883-2 (1-690) x US-09-811-115-1 (1-9274)	Best Local Similarity: 40.43% Mismatches: 31 • • Query Match: 738 Indels: 738 DB: 10 Gaps: 6	Similarity: 41.128 Conservative: 9

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	_	3717 CTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATC 3776
Db 4797 TATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGGGGGCATG 4856	• •	
Qy 330GlyAlaGlyGlyMet 334		
Db 4737 ACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGATGCTGAGGAG 4796	· · . ·	
Qy 329 329	•	329 329
46// CCCAGCGCTTTGTGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	•	3597 TGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGATGACAAGGGCTGC 3656
		329 329
379		3537 GGTGTGAAACCTGACCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAGGGGCGCA 3596
Db 4617 TCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGGCATGGCCAGGGAC 4676		329 329
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Db 4557 CAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATGATTGAC 4616		
Qy 329 329		
Db 4497 TACGATGGGATCCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAAGGGGGGAGCGGCTGCCC 4556		TGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAGGCTGAC
Qy 329		329 329
4437 AGTGATGTGGAGTTATGGTGTGACTGTGGGAGCTGATGACTTTTGGGGCCAAACCT		3357 GAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGTTTGCCG 3416
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		3297 CCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGGCCAGGAGTGCGTGGAG 3356
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		3117 AGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCACACGGTGCCCTGG 3176
4197		329 329
Qy 329 329		3057 CTGACCCTGCAAGGGCTGGGCATCAGCTGGGCTGGGGCTCACTGAGGGAACTGGGC 3116
Db 4137 TATEGCTGCCTCTTAGACCATGTCCGGGGAAAACCGCGGGGCCTGGGCCTCCCAGGACCTG 4196		
Qy . 329 329		
Db 4077 TCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTTATGCCC 4136		2997 AGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGCCTACTCG 3056
5 2 3	-	329 329
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Db 3957 GGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCCCCCAAA 4016		329
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Sequence 5, Application US/09441411
Publication No. US2003008342A1
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Indegerd
APPLICANT: Hellstrom, Karl Erik
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                                      SEQ
                                             CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                           APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erlk
TITLE OF INVENTION: SURFACE RECEPTOR
FILE REFERENCE: 730033.409
LENGTH: 4473
TYPE: DNA
ORGANISM: Homo sapiens
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                                                     PheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla
                          CysLysGlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThr
                                                                                                                                             LeuAlaLeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMet
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3169 CCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTG 3228	Db .	2089 GACAAGGGCTGCCCGGCCGAGCAGAGAGAGCCACCCCTCTGACGTCCATCATCTCTGCGGTG 2148
329 329	Оу	
3109 ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	dd	GAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCCACTCCTGTGTGGACCTGGAT
329 329	Qy	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3049 TGGATGATTGACTÇTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGC 3108	Db	CGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCCATCTGGAAGTTTCCAGAT
329 329	Qy	
2989 GAGCGGCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT 3048	. Db	CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT
329 329	Qy	
2929 GGGGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGG 2988	dd	CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGCCTCAGTGACCTGTTTTGGA
329	Qy	
2869 TTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGGAGCTGATGACTTTT 2928	dd	GAGTGCGT6GAGGAATGCCGAGTACTGCAGGGGCTCCCAGGGAGTATGTGAATGCCAGG
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2809 GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG 2868	םם	こう かいがい かいがい かい かい こうしょう アン・カン・カン・カン・カン・カン・カン・カン・カン・カン・カン・カン・カン・カン
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2749 GTCAAAATTACAGACTTCGGGCTGGCTGCTGCTGGACATTGACGAGACAGAGTACCAT 2808	da	CORPORAÇÃO A CARACITATO A COLOTO CONTRACA DE SERVIDA COLOTO CONTRACA COLOTO COL
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2689 GTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAT 2748	Db	ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC
329 329	Qy	
2629 TCCCAGGACCTGCTGAACTGGTGTATGCCAGATTGCCAAGGGGATGAGCTACCTGGAGGAT 2688.	Db	AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC
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2569 CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAAACCGCGGACGCCTGGGC 2628	Db	GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTG
329 329	Qy	
2509 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA 2568	Db	CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAAT
329 329	Qy	
2449 ACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC 2508	db dd	СТАТТТАКАСАСТСТСКАЛАКАСАТСАСАТТАССТАТАСАТАСАССАТСТСТСАССТВОТО СТАТТТАСАСАСТСТСТСКАЛАСАСТСТВОТОТАТТАССТВОТАСТСТВОТОТОТОТОТОТОТОТОТОТОТОТОТОТОТОТОТО
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2389 TGGATCCCTGATGGGGAGAATGTGAAAATTCCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2448	dd	GAGAGCTTTGATGGGGACCCAGCCTGCAACACTGCCCGCTCCAGGCAGCGAGCAGCTACCTCCAA
329 329 .	Оу	
2329 GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATC 2388	Db	GCCAATATCCAGGAGTTTGCTGGCTGGCAAGAAGATCTTTGGGAAGCCTTGGCATTTTCTGCCA
329 329	Qy	
2269 CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG 2328	ממ	GCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGT
329 329	Qy	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
2209 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG 2268	Db	ACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGT
329 329	Qy	
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Length:
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APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENENT .073A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-05
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 3768
TYPE: DNA
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Patent No. US20020001587A1
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                                                                                                                                                                      GlnArgAsnProGlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLys
                                                                                                                                                                                                                                                                                                                                          GlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIle
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                                                                                                                                TGCCATGAGCAGTGTGCTGCCGGCTGCACGGGCCCCAAGCACTCTGACTGCCTGGCCTGC
                                                                                                                                          CysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCys
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330GlyAlaGlyGlyMetValHisHisArgHisArgSerSerSerSerThrArgSerGly 347	·	329 329
3046 GACCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCT 3105	da	TCTGCGGTGGTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATC
329 329	Qy	
2986 CCAGCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGG 3045	da	GACCTGGATGACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCC
329 329	Qy	
2926 TTCTCCCGCATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGC 2985	Db	TTTCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTG
329 329	Qy	329 329
GTCAAATGTTGGATGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAA	Db	TGCGTGGCCCGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCCATCTGGAAG
329 329	. Oy	
2806 GAAAAGGGGGAGCGGCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATGATCATG 2865	Db	TGTTTTGGACCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTÀTAAGGACCCTCCCTTC
329 329	. Oy	
2746 ATGACTTTTGGGGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTG 2805	Db	AATGCCAGGCACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACC
329 329	Qy	
2686 CGCCGGCGGTTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTG 2745	рь	CGGGGCCAGGAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTG
329 329	Qy	
2626 GAGTACCATGCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTC 2685	Db	1546 GCCCGAGGGCACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTT 1605
329	Qy	329 329
CCCAACCATGTCAAAATTACAGACTTCGGGCTGGCTGGCT	<u>D</u> b	1486 ACTGCCAACCGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGC 1545
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2326 GGTGTGGGCTCCCCATATGTCTCCCGGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAG 2385	Db Db	
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APPLICANT: KING, Kathleen
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TU
FILE REFERENCE: GENENT.034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
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Alignment Scores:	PD) of human HER-2/neu	red portion	OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu NAME/KEY: misc feature		LOCATION: (2026)(3765) OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu	OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu NAME/KEY: misc_feature		OTHER INFORMATION: human HER-2/neu protein	NAME/KEY: CDS	ORGANISM: Homo sapiens FEATURE:	TYPE: DNA	SEQ ID NO 9	NUMBER OF SEQ ID NOS: 26	PRIOR APPLICATION NUMBER: US 60/117,976 PRIOR FILING DATE: 1999-01-29	PRIOR APPLICATION NUMBER: US 09/493,480 PRIOR FILING DATE: 2000-01-28	CURRENT FILING DATE: 2001-05-09	FILE REFERENCE: 014058-009810PC GIIDDENIT ADDITION WINDERS 17/00/061-266	APPLICANT: SmithKline Beecham Biologicals S. A.	APPLICANT: Gheyen, matri A. APPLICANT: Gheyen, matri A. APPLICANT: Greyen, matri	GENERAL INFORMATION: Cotto	-09-854-356-9, Application US/09854356	RESULT 12	ACCTTCAAAGGGACACCTACGGCAGAGAACCCAGAGTACCTGGGCTCTGGACGTGCCA	546	Db 3646 GCCTTCGACAACCTCTATTACTGGGACCAGGACCCAGAGCGGGGGGCTCCACCCAGC 3705			TvrLeuThrProGlnGlvGlvAlaAlaProGlnProHisProProProAlapheSerPro	GGAAGAATGGGGTCGTCAAAGACGTTTTTGCCTTTGGGGGTGCCGTGGAGAACCCCCGAG	468 GlyLysAsnGlyValValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGlu		ProLeuProAlaAlaArgProAlaGlvAlaThrLeuGluArgAlaLvsThrLeuSerPro	3406 CAGCCTGAATATGTGAACCAGCTCAGATGTTTTTTTTTT	428 GlnproGlijeurVallaandinbroaanVallarubrothobriococcoccistococcocc		Drothryal Drof.eu Droserciumbraenciumurualaladrof.umbrouccorpro
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CA 2	GATATCCAGGAGGTGCAGGGCTACGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCC	b 226	DЬ
ro 1:	IleGlnGluValGlnGlyTyrValLeuIleAlaHisAsnGlnValA	у 95	γQ
AG 2:	ValGlnGlyAsnLeuGluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuG 	y 75 b 166	Qy Db
ଦ	GCCAGTCCCGAGACCCACCTGGACATGCTCCGCCACCTCTACCAGGGCTGCCAC	10	Д
	ProAlaSerProGluThrH1sLeuAspMetLeuArgH1sLeuTyrGlnGlyCysGlnVa	Ui	Qy
Leu 5	LeuAlaArgGlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgL 	у 35 b 46	Qy Db
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	329	ANGUGACUGUAGANGATUCUGAAGTAUAAUGATGUGGAGAUTGUTGCAGGAAAUGGAG	Qy 329
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	2025	TCTGCGGTGGTTGGCATTCTGCTGGTCGTCGTCTTTGGGGGTGGTCTTTGGGATCCTCATC	Db 1966
	329		Оу 329
	1965	GACCTGGATGACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCC	Db 1906
	329		Qу 329
-	1905	TTTCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTG	Db 1846
	329		Оу 329
	1845	TGCGTGGCCCGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCCATCTGGAAG	Db 1786
	329		Оу 329
	1785	TGTTTTGGACCGGAGGCTGACCAGTGTGTGGCCCTGTGCCCACTATAAGGACCCCTCCCT	Db 1726
	329		Оу 329
-	1725	AATGCCAGGCACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACC	Db 1666
	329		Оу 329
	1665	CGGGGCCAGGAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCCAGGGAGTATGTG	1606 ממ
	329		Оу 329
	1605	GCCCGAGGGCACTGCTGGGGTCCAGGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTT	Db 1546
٠	329		Оу 329
	1545	ACTGCCAACCGGCCAGAGGACGAGTGTGTGGGGCGAGGGCCTGGCCTGCCACCAGCTGTGC	Db 1486
	329		Оу 329
	1485	TTCGTGCACACGGTGCCCTGGGACCAGCTCTTTCGGAACCCCGCACCAAGCTCTGCTCCAC	Db 1426
-	329		Оу 329
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	329		Оу 329
	1125	GTTACCAGTGCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCA	Db 1066
-	329		Оу 329
	1065	AAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCA	Db 1006
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Db 2086 CTGGTIGGAGCCGCTGACACCTACGGAGCGATGCCCAAGCGGGGGGAGATGCGGATCCTG 2145 Qy 329																			_																
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Sequence 1, Application US/09930125

Publication No. US20020193329A1

GENERAL INFORMATION:

APPLICANT: Hand-Zimmerman, Susan
APPLICANT: Cheever, Martin A.

APPLICANT: Lodes, Michael J.

APPLICANT: Kalos, Michael J.

APPLICANT: Kalos, Michael D.

APPLICANT: McNeill, Patricia D.

APPLICANT: McNeill, Patricia D.

APPLICANT: Wedvick, Thomas S.

TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOI TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MAI FILE REFERENCE: 210121.544

CURRENT APPLICATION NUMBER: US/09/930,125

CURRENT APPLICATION NUMBER: US/09/930,125

CURRENT APPLICATION STORM NUMBER OF SEQ ID NOS: 25

SOFTMARE: FRAFTER OF SEQ ID NOS: 25

SOFTMARE: FRAFTER OF SEG ID NOS: 25
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NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
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LOCATION: (1)...(3765)
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CysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCys
                                                                                                                                                                                                 ThrArgThrValCysAlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCys
                                                                                                                                                                                                                       GlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIle
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AAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCA
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368 AlaProSerGluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAla 	Qy Db	·	329 329 2146 AAAGAGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTAC 2205
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	ον σα		329 329 2026 AAGCGACGGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAG 2085
3046 GACCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCT 330GlyAlaGlyGlyMetValHisHisArqHisArqSerSerThrArqSerGly	OV Db		1966 TCTGCGGTGGTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATC 2025
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2986 CCAGCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGG	da		GACCTGGATGACAAGGGCTGCCCCCCCCGAGCAGAGAGCCAGCC
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2926 TTCTCCCGCATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGC	Db		TTTCCAGATGAGGAGGCCCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTG
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2866 GTCAAATGTTGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAA	Db		うく ペンション・ロイン・ロイン・ロイン・ロー・ロー・ロー・ロー・ロー・ロー・ロー・ロー・ロー・ロー・ロー・ロー・ロー・
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2626 GAGTACCATGCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTC	da		GCCCGAGGGCACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTT
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2566 CCCAACCATGTCAAAATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTGACGAGACA	 Db		1486 ACTGCCAACCGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGC 1545
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2506 CTGGAGGATGTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGT	da d		1426 TTCGTGCACACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCAC 1485
329	Оу		
2446 CGCCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTAC	da		CGCTCACTGAGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACC
329	Qy		
2386 CTGGTGACACAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGA	. Db	, r .	CTGCACAATGGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTG
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2266 AGGGAAAACACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCT	ДD		CAGCTCCAAGTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGG
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2206 AAGGGCATCTGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTG	Db		TTTCTGCCGGAGAGCTTTGATGGGGACCCTCGAGCTCTACCACCTCCCTC
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                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                       APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                        Patent No. US20020061310A1
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 10
LENGTH: 1437
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RESULT 15
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               APPLICANT: Corixa Corporation
APPLICANT: SmithKilne Beecham Biologicals
TITLE OF INVENTION: HER-Z/neu Fusion Protei
FILE REFERENCE: 014058-009810PC
                                                                               APPLICANT: Cheever, Martin A. APPLICANT: Gheysen, Dirk
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NUMBER: US/09/854,356
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Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.1
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LOCATION: (2999)..(3796)
OTHER INFORMATION: phosphorylation
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LOCATION: (2188)..(3022)
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LOCATION: (2057)..(3796)
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OTHER INFORMATION: extracellular
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LOCATION: (26)..(3799)
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Conservative:
Mismatches:
Indels:
Gaps:
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1474	AGTGGATTGGCTCTGATTCACCGCAACGCCCATCTCTGCTTTGTACACACTGTACCTTGG	1415	용
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1414	TTGACACTGCAAGGCCTGGGGATCCACTCGCTGGGGCTGCGCTCACTGCGGGAGCTGGGC	1355	ф
329		329	Ş
1354	AGTGTCTTCCAGAACCTTCGAATCATTCGGGGACGGATTCTCCACGATGGCGCGTACTCA	1295	В
329		329	οy
1294	$\tt CTGGAGGAGATCACAGGTTACCTGTACATCTCAGCATGGCCAGACAGTCTCCGTGACCTC$	1235	В
329		329	γ
1234	GGGGACCCCTCCTCCGGCATTGCTCCGCTGAGGCCTGAGCAGCTCCAAGTGTTCGAAACC	1175	В
329		329	Qy
1174	GAGTTTGATGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTTTGCCGGAGAGCTTTGAT	1115	В
329		329	Q
 1114	TATGGTCTGGGCATGGAGCACCTTCGAGGGGGCGAGGGCCATCACCAGTGACAATGTCCAG	1055	Ъ
329 ·		329	γo
1054	ACAGCTGAGGACGGAACACAGCGTTGTGAGAAATGCAGCAAGCCCTGTGCTCGAGTGTGC	995	В
329		329	Qy
994	TACCTGTCTACGGAAGTGGGATCCTGCACTCTGGTGTGTCCCCCGAATAACCAAGAGGTC	935	Дb
329	yrLeuSerThrAspValGl	322	γo
934	CACAACCCTGAGGGTCGCTACACCTTTGGTGCCCAGCTGCGTGACCACCTGCCCCTACAAC	875	дb
321	nProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysProTyr	302	γo
874	ATCTGTGAGCTGCACTGCCCAGCCCTCGTCACCTACAACACAGACACCTTTGAGTCCATG	815	B
301	CysGluLeuH1sCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMe	282	γo
814	GACTGCCTGGCCTGCCTCCACTTCAATCATAGTGG	755	용
281	lyCysThrGlyProLysH1sSerAspCysLeuAlaCysLeuH1sPheAsnH1sSerG	262	γo
5		9	망
261	lyCysAlaArgCysLysGlyProLeuProThrAspCvsCysHisGluGlnCvsAla	242	Ş
694	CACTGTTGGGGTGAGAGTCCGGAAGACTGTCAGATCTTGACTGGCACCATCTGTACCAGT	635	용 5
634	ATATAGACACCAATCGTTCCCGGGCCTGTCCACCTTGTGCCCCCCGCCTGCAAAGACAA	, 7	문
221	rAsnArgSerArgAlaCysH1sProCysSerProMetCysLysGly	0	δ
574	ACCAGGACATGGTTTTGTGGAAGGACGTCTTCCGCAAGAATAACCAACTGGC	515	Ъ
201	ThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeu	182	Qγ
181 514	ArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeuCys	455	8 8
454	ACAATGTCGCCGCCTCCACCCCAGGCAGAACCCCAGAGGGGCTGCGGGAGCTGC	و ۱	망

GTACACAGGGACCTGGCTGCCCGGAATGTGCTAGTCAAGAGTCCCAACCACGTCAAGATT		Db .
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CAAGGGGATGAGCTACCT	2495 CTGCTCAACTGGTGTGTTCAGATTGCCAAGGGGATGAGCTACCTGGAGGAĊGTGCGGCTT	Db .
	329	Qy
PCCGAGAACACCGAGGTCG	2435 CCCTACGGCTGCCTTCTGGACCATGTCCGAGAACACCGAGGTCGCCTAGGCTCCCAGGAC	뫄 :
	329	Qy
"GACATCCACAGTACAG	2375 GTGTCCCGCCTCCTGGGCATCTGCCTGACATCCACAGTACAGCTGGTGACACAGCTTATG	Db :
	329	Qy
\AGCGTATGTGATGGCT	2315 AAAGCCAACAAAGAAATTCTAGATGAAGCGTATGTGATGGCTGGTGTGGGTTCTCCGTAT	<u>В</u>
	329	Qy
rggctatcaaggtgtt	2255 GATGGGGAGAATGTGAAAATCCCCGTGGCTATCAAGGTGTTGAGAGAAAACACATCTCCT	В
	329	Ωу
CTTTTGGCACTGTCTA	2195 AAGGTGAAGGTGCTTGGATCAGGAGCTTTTGGCACTGTCTACAAGGGCATCTGGATCCCA	В
	329	Оу
STCAGATGCGGATCCT	2135 CCCAGCGGAGCAATGCCCAACCAGGCTCAGATGCGGATCCTAAAAGAGACGGAGCTAAGG	Db
	329	Qy
rgctgcaggaaactga	2075 ATCCGGAAGTATACGATGCGTAGGCTGCTGCAGGAAACTGAGTTAGTGGAGCCGCTGACG	망
	329	Qy
rcgttggaatcctaat	2015 CTGCTGTTCCTGATCTTAGTGGTGGTCGTTGGAATCCTAATCAAACGAAGGAGACAGAAG	В
	329	Qy
CGGTGACATTCATCA	1955 TGCCCAGCAGAGCAGAGCCAGCCCGGTGACATTCATCATTGCAACTGTAGAGGGCGTC	В
	329	Ωу
3CACCCACTCCTGTGT	1895 ATATGCCAGCCGTGCCCCATCAACTGCACCCACTCCTGTGTGGGATCTGGATGAACGAGGC	рь
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ACATGCCCATCTGGAA	1835 AGTGGTGTGAAACCGGACCTCTCCTACATGCCCCATCTGGAAGTACCCGGATGAGGAGGGC	₽
	329	Qy
ACAAGGACTCGTCCT	1775 GATCAGTGTGCAGCCTGCGCCCACTACAAGGACTCGTCCTCCTGTGTGGCCTCGCTGCCCC	В
	329	Qy
\AAACAGCTCAGAGA(1715 CCGTGTCACCCCGAGTGTCAGCCTCAAAACAGCTCAGAGACCTGCTTTGGATCGGAGGCT	В
	329	Qy
rccccgggagtatg	1655 GAGGAGTGCCGAGTATGGAAGGGGCTCCCCCGGGAGTATGTGAGTGA	₽
	329	Qy
ACTGCAGTCATTTCC	1595 GGGCCAGGGCCCACCCAGTGTGTCAACTGCAGTCATTTCCTTCGGGGCCAGGAGTGTGTG	8.
	329	Qy
rctgtaactcactgtg	1535 GACTTGTGCGTCTCGAGCGGCTTGGTCTGTAACTCACTGTGTGCCCCACGGGCACTGCTGG	ф
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\GGCCCTGCTCCACAGT	1475 GACCAGCTCTTCCGGAACCCACATCAGGCCCTGCTCCACAGTGGGAACCGGCCGG	В

ş	Эу 329		329	
မွ	Db 2615 ACAGATTTCGGGCTGGCTCGGCTG	CTGGACATTGATGAGACAGAGTACCATGCAGATGGG	2674	•
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ğ	Db 2675 GGCAAGGTGCCCATCAAATGGATG	GCATTGGAATCTATTCTCAGACGCCGGTTCACCCAT	2734	
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ğ	Db 2735 CAGAGTGATGTGTGGAGCTATGGA	TGATGAC	2794	
¥	λy 329 ·····		329	
8	CCCAGC	TCCCTGATTTGCTGGAGAAGGG	2854	
¥	ру 329		329	
8	Db 2855 CCTCAGCCTCCAATCTGCACCATT	GATGTCTACATGATTATGGTCAAATGTTGGATGATT	2914	
Ŋ	Эу 329		329	
8	Db 2915 GACTCTGAATGTCGCCCGAGATTC	CGGGAGTTGGTGTCAGAATTTTCACGTATGGCGAGG	2974	
у	Эу 329		329	
မွ	Db 2975 GACCCCCAGCGTTTTGTGGTCATC	CAGAACGAGGACTTGGGCCCATCCAGCCCCATGGAC	3034	
γ	2y 329		329	
g	Db 3035 AGTACCTTCTACCGTTCACTGCTG	GAAGATGATGACATGGGTGACCTGGTAGACGCTGAA	3094	
Ϋ́	2y 330	G1	333	
မ	Db 3095 GAGTATCTGGTGCCCCAGCAGGGA	CAGGCACTGG	3154	
ý	Dy 334 MetValHisHisArgHisArgSer	SerSerThrArgSerGlyGlyGlyAspLeuThrLeu	353	
b	ATAGAAGGCACCGCAG	CGTCCACCAGGAGTGGAGGTGGAGCTGACACT	3214	
ν	2y 354 GlyLeuGluProSerGluGluGlu	AlaProArgSerProLeuAlaProSerGluGlyAla	373	
9	3215 GGCCTGGAGCCCTCGGAAGAAGGG	CCCCCAGATCTCCACTGGCTCCCTCGGAAGGGG	32	
Ş	374 GlySerAspValPheAspGlyAsp	LeuGlyMetGlyAlaAlaLysGlyLeuGlnSerLeu	393	
용	3275 GGCTCCGATGTGTTTGATGGTGAC	CTGGCAATGGGGGTAACCAAAGGGCTGCAGAGCC	3334	
ν	394 ProThrHisAspP	GlnArgTyrSerGluAspProThrValProLeuPro	. <u>1</u> 3	٠
Ď	3335 TCTCCACATGACCTCAGCCCTCT	AGCGGTACAGCGAGGACCCCACATTACCTCTGCC	3394	
5 5	414 S	ProLeuThrCysSerProGlnProGluTyrValAsn	ω	
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3 5	434 GinProAspValArgProGinPr	OPTOSerProArgGluGlyProLeuProAlaAlaArg 	3514	
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음 <i>첫</i>	Qy 454 ProAlaGlyAlaThrLeuGluArg	gAlaLysThrLeuSerProGlyLysAsnGlyValVal	473 3574	•
υγ	474 LysaspValPheAlaPheGlyGly	aValGluAsnProGluTyrLeuThrProGln	493	
8	ACGTTTTTGCCTTCGGGGG	TGGAGAACCCTGAATACTTAGTACCGA	3634	
υ	494 GlyAlaAlaProGl	ProProAlaPheSerProAlaPheAspAsnLeuTyr	513	
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earch co				·		у 534		
Search completed: May 8, 2003, 14:57:36 Job time: 285 secs	3875 AGGGTC 3880	563 HisVal 564 .	3815 CCTGTGCTTTCAGAGTGGGGAAGGCCTGACTTGTGGTCTCCATCGCCACAAAGCAGGAG 387	554 ProSerProSerThrGlnProTrpGlu 562	3755 ACTGCAGAGAACCCTGAGTACCTAGGCCTGGATGTACCTGTATGAGACGTGTGCAGACGT 381	ThralaGluAsnProGluTyrLeuGlyLeuAspValProAlaAlaAlaProAlaArgSer 553	3695 TACTGGGACCAGAACTCATCGGAGCAGGGGCCTCCACCAAGTAACTTTGAAGGGACCCCC 375	514 TyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThrPro 533
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Result
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-DB-Issued_patents_NA -QFMT-fastap -SUFFIX-pDn.rni -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT=0 -UNITS-blts -START=1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15
-MODE-LOCAL -OUTEMT-pto -NORM-ext -HEARSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09821883 -GCORE-SURVANA - CONTROL - 
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                               258.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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US-08-645-865-9
US-09-167-322-4
US-09-048-804-1
US-09-055-101-1
US-08-625-101-1
US-08-526-786-1
US-08-146-283-3
US-08-229-515A-14
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US-08-318-193	PCT-US95-01185-6	US-08-762-227A-	US-08-446-872A-6	US-08-468-609A-6	US-08-469-318-66	PCT-US95-01185-6	US-08-762-227A-	US-08-446-872A-6	US-08-468-609A-6	US-08-469-318-6	US-09-570-454-	US-09-630-706-	US-08-475-352-	US-08-473-119-	US-07-978-895-	US-08-318-193-	5200327	US-08-484-43	US-08-484-438-	US-09-632-58	US-08-318-193-	5200327-2	US-09-676-610B	US-08-475-0	US-09-676-610B-2	-60-sn	US-08-658-883B-	US-09-344-19	US-08-579-823A	us-09-146-283-	-08-422-734	US-08-422-108-
 e 1, A	nence 66,	equence	e 66,	e 66,	equence 66,	uence 69,	equence 69,	equence 69,	equence 69,	e 69,	equence 1, A	equence 3, A	ω		'n	equence 9,		ი ა	Sequence 1, Appli	ω	Sequence 7, Appli		e 17, Ap	equence 3,	equence 25, Ap	equence 26, Ap	e 1, Ap	equence 1, App	e 1, App	e 1, Ap	equence 2, Ap	Sequence 2, Appli

ALIGNMENTS

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Sequence 9, Application US/08229515A Patent No. 5518885
                                    TELEFAX: 404-688-9880 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                        REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RAZIUDDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pair
                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           APPLICATION NUMBER: US/08/229,515A FILING DATE: 19 APR 1994
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-229-515A-9
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DB:
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                   AsnHisSerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThr
                                                                         LeuAlaLeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMet
                                                                                                                                                        ASTLEUGluLeUThTTYTLEUPTOTHTASTAlaSETLEUSETPHELEUGlTASPILEGIT
                                                                                                                                                                                                                                                                                            CCCCAGCTCTGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAG
                                                                                                                                    ProGlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGln
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329		329	Qy
2004	CGCTGCCCCAGCGGTGTGAAACCTGACCTCCTACATGCCCATCTGGAAGTTTCCCAGAT	1945	Db
329		329	Qy
1944	CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT	1885	дд
329	3	329	Qy
1884	CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA	1825	Db
329	3	329	Qy
1824	GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGG	1765	Db
329	3	329	Qy
1764	CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG	1705	Db
329	9	32	Оу
1704	5 CGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCGAGGG	164	Db
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1644	ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC 1	1585	Db
329		329	Qy
1584	AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC	1525	ДĎ
329		329	Оу
1524	5 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGGCTGGGGCTGCGCTCACTG	146	Db
329		329	Qy
1464	CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAAT	1405	Дb
329	· · ·	329	Оу
1404	GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC	1345	Дb
329	9	32	Qy
1344	GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG	1285	dg.
329		329	γQ
1284	GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG	1225	ф
329		329	Qy
1224	5 GCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGT	116	фd
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1164	AACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGT	1105	đđ
329		329	Qy
11:04	TGTCCCTACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCCCCTGCAC	1045	ф
329	CysProTyrAsnTyrLeuSerThrAspValGlySer	318	Qy
1044	5 TITGAGTCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCCAGCTGTGTGACTGCC	98	Db
317	PheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla	298	Qy
984	AACCACAGTGGCATCTGTGAGCTGCACTGCCCAGCCCTGGTCACCTACAACACAGAGACACG	925	

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	STATE: Georgia COUNTRY: usa ZIP: 30303		3085 ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG
200	EDLE & ROSENBERG PC eachtree Street, Suite 1		3025 TGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGC 3084
	OF SEQUENCES: 19 PONDENCE ADDRESS:		
ING PROTEIN IN	TITLE OF INVENTION: REBEZ PROMOTER BINDING TITLE OF INVENTION: NEOPLASTIC DISEASE		2965 GAGCGGCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT 3024
	GENERAL INFORMATION: APPLICANT: RAZIUDDIN APPLICANT: RAZIUDDIN		329 329
	9, A	; Se	2905 GGGGCCAAACCTTACGATGGGATCCCCAGCCCGGGAGATCCCCTGACCTGCTGGAAAAGGGG 2964
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)19 ACCAG	Db	2845 TTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGACTTTT 2904
. :	AlaArgSerProSerPro	Qy	329 329
TOTGGACGTGCCA	GGGAC		2785 GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCCGCCGGCGG 2844
yLeuAspValProAlaAla 		Qy Oy	329 329
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ICCTGCCITCAGCCCAGCCT			2665 GTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAT 2724
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aValGluAsnProGluTyrL		Qy	329 329
CAAGACTCTCTCCCCAGGG	GCTGC	Db	2545 CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGGAAAACCGCGGGACGCCTGGGC 2604
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uGlyMetGlyAlaAlaLys(371 GluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu	Qy	329 329
CCCCAGGTCTCCACTGGCA	3325 CTGACACTAGGGCTGGAGCCCTCTGAAGAGGAGGCC	Db	2245 CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG 2304
aProArgSerProLeuAlai		Qy	329 329
ATCTACCAGGAGTGGCGGT0		Db	2185 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG 2244
rSerThrArgSerGlyGly(331 AlaGlyGlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyAsp	Qy	329 329
CTTCTGTCCAGACCCTGCC	3205 GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGC	Db	2125 GTTGGCATTCTGCTGGTCGTCGTCGTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGG 2184
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GGACGATGACATGGGGGAC	3145 CCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTG	Db	2065 GACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTG 2124
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: PERRYMAN, DAVID 6
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-9770
TELEFAX: 404-688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
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ASGG1yASpProLeuASnASnThrThrProValThrG1yAlaSerProG1yG1yLeuArg
                                                                                                                                  AsnLeuGluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGln
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TYPE: Floppy disk
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22 CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGGCCAG	CGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCGAGGG 17	32	ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCAÇACTGCCAAC 16	32	AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 15	3:	GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTG	32	CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAAT 14	3:	GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 14	32	GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG	32	ATTTCTGCCG	3:	GCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGT 1	32	AACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGT 11	3	TGTCCCTACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCCCCTGCAC 11	sProTyrAsnTyrLeuSerThrAspValGlySer 3	TGCC 1	heGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla 3	AACCACAGTGGCATCTGTGAGCTGCCACTGCCCAGCCCTGGTCACCTACAACACAGACACG 9	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThr 2	9	lncy	8	isGlu 2	TGTAAGGGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTGTCAGAGCCTÇACGCGCACT 80	31ySerArgCysTrpG1yG1uSerSerG1uAspCysG1nSerLeuThrArg	CTGGCTCTCACACTGATAGACACCAACCGCTCTCGGGGCCTGCCACCCCTGTTCTCCGGATG 7.	nArgSerArgAlaCysHisProCysSerProMet
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531 GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProAlaAlaAlaPro 550	Qy	329
511 AsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLys 530	Ob	
CCCAGGGAGGAGCTGCCCTCAGCCCACCCTCCTCCTCCTCAGCCCAGCCTTCGAC	da	2665 GTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAT 2724
491 ProGlnGlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAsp 510	Qy	TCCCAGGACCTGCTGAACTGGTGTATGCCAGATTGCCAAGGGGATGAGCTACCTGGAGGAT
471 GlyvalValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThr 490	Oy Db	
451 AlaAlaArgProAlaGlyAlaThrLeuGluArgAlaLysThrLeuSerProGlyLysAsn 470	Qy Db	CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGC
431 TYPVBLASNGINPTOASPVBLARGPTOGTNPTOPTOSETPTOATGCTUG_PTOLEUPTO 450	Db	329 329 2485 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA 2544
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ProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGluProGlu	Qy	2365 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2424
391 GlnSerLeuproThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal 410	Qy	329 329
3385 GAAGGGGCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTG 3444	Db	2305 GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCGTTTTGGCACGAGTCTACAAGGGCATC 2364
371 GluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 390	Qy	CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG
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AlaG1yG1yMetValHisHisArgHisArgSerSerSerThrArgSerG1yG1yG1yAsp	Qy	329 329
3205 GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCCTGCCCCGGGC 3264 : ;	Db	のうさん いっしょう はんしゅく しゅく しゅうしゅう はんしゅう しゅうじゅう しゅうしゅう しゅう
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2965 GAGCGGCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT 3024	Db	1885 CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT
329 329	У	1023 CACIBILIBUCHAUCHIBABIBICABCCUCABAANIBBCICABIBACCIBITIIBBA 1884
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329 329	Qy	GAGTGCGTGGAGGAATGCCGAGGGGCTCCCCCAGGGAGTATGTGAATGCCAGG
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Best Local Similarity:
                                                                                                                                                                                                                                                                                  Score:
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                                                                                                                                                                                                                                                                                                                                                     NAME: MONACO, DANIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5349
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application Patent No. 6365151 GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
OCT. 1998
CLASSIFICATION DATA:
OCT. 1998
CLASSIFICATION DATA:
OCT. 1998
CLASSIFICATION DATA:
OCT. 1998
CLASSIFICATION DATA:
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ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco,
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. England, James M. ITITLE OF INVENTION: CANCER VACCINE
          GlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSer
                                                                                                             GAGCTGGCGGCCTTGTGCCGCTGG-----
                                                                                                                                                                                   ArgAlaAlaProLeuLeuLeuAlaArgAla----
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                        GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC
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                                                 Pred.
                                                            Alignment Scores
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                                                                                                                      TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 4473 base pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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NAME: Paul K. Legaard
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                                                                                                            TYPE: Nucleion STRANDEDNESS:
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                                                                                                   TOPOLOGY:
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		2208	GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGTCTTTGGGATCCTCATCAAGCGACGG	2149	В
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		2148	GACAAGGGCTGCCCGCCGAGCAGAGAGCCCAGCCCTCTGACGTCCATCATCTCTGCGGTG	2089	B
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		2088	GAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGAT	2029	밁
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		2028	CGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGAT	1969	밁
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		1248	GCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGT	1189	В
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 Best Local Similarity:
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TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEO ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
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TGTCCCTACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCCCCTGCAC
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	331 AlaGlvGlvMotValHisArgHisArgSorSorThrArgSorGlvGlvGlvAsp		2149 GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGG 2208
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•	330		2089 GACAAGGGCTGCCCCGCCGAGCAGAGAGCCCAÇCCCTCTGACGTCCATCATCTCTGCGGTG 2148
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	2749 GTCAAAATTACAGACTTCGGGCTGGCTCGGCTGGACATTGACGAGACAGAGTACCAT		1669 CGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCGAGGG 1728
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	2007 BIBCBBCICBIACHCHBBBACIIBBCCBCICBBANCBIBCIBBICANBHBICCHI		1609 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCCGCACCAAGCTCTGCTCCACACTGCCAAC 1668
			329 329
	2629 TCCCAGGACCTGCTGAACTGGTGTATGCCAAAGGGGATGAGCTACCTGGAGGAT		1549 AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 1608
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	270		1489 GGCGCCTACTCGCTGACCCTGCAAGGGCCTGGGCATCAGCTGGCCTGGGGGCTGCGCTCACTG 1548
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	2009 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACA		1429 CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGGACGAATTCTGCACAAT 1488
	329		329 329
	2449 ACATCCCCCAAAGCCAACAAAGAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC		1369 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 1428
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	2389 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC		1309 GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG
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	2329 GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTTGGCACAGTCTACAAGGGCATC		1249 GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG 1308
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                                                                                                                                                                                              Sequence 1, Application US/08625101

Patent No. 5869445

GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.

TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2

TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BE
STREET: 6300 Columbia
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          APPLICATION NUMBER: FILING DATE: 01-APPLICATION: 424
                                                                                                                             STREET: 6300 Colur
CITY: Seattle
STATE: Washington
                                                                                                           ZIP: 98104-7092
                                                                                                                     COUNTRY:
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  INFORMATION
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Best Local Similarity:
Query Match:
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; LOCATION:
US-08-625-101-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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CysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCys
                                           ThrArgThrValCysAlaGlyGlyCysAlaArgCysLySGlyProLeuProThrAspCys
                                                                          LeuGlnArgLeuArgIleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAla
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                               GTGCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCAGGA
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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2866 GTCAAATGTTGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAA 2925	ДĎ	1786 TGCGTGGCCCGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAG 1845
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	D 10	1666 AATGCCAGGCACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACC 1725
46 ATGACTTTTGGGGCCAAACCTTACGATGGGATCCCCAGCCCGGGAGATCCCTGACCTGCTG	dd 1	329 329
329		1606 CGGGGCCAGGAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGGCTCCCCCAGGGAGTATGTG 1665
2586 CGCCGGCGGTTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTG 2745	Db	329 329
329 329	Qy	GCCCRARGACTACTACTACACCCACCCACTATATATATACTACACCCAGTTCCTT
2626 GAGTACCATGCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTC 2685	dd	・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・
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2566 CCCAACCATGTCAAAATTACAGACTTCGGGCTGGCTGGCT	Db	ACTGCCAACCGGCCAGAGGACGAGTGTGTGGGGCGAGGGGCCTGGCCTGCCAGCTGTGC 1
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2506 CTGGAGGATGTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGT 2565	מם סט	TTCGTGCACACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCAC
329 329		329
2446 CGCCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTAC 2505	. 06	1366 CGCTCACTGAGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGC 1425
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2326 GGTGTGGGCTCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAG 2385	Db	
329	Qy	329 329
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2146 AAAGAGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTTGGCACAGTCTAC 2205 :.	da	329
329 329	Qy	AAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCA
2086 CTGGTGGAGCCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTG 2145 : .	Db	
329 329	. Qy	
2026 AAGCGACGGCAGCAGAAGATCCGGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAG 2085	Db	6 CCCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACACAGGGTGTGAGAAGTGCAGC 1
329 329	Qy	29
1966 TCTGCGGTGGTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGAICCTCATC 2025	Db	
329 329	Oy	ValThrAlaCysProTyrAsnTyrLeuSerThrAspValGlySer
1906 GACCTGGATGACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCC	da	ACAGACACGTTTGAGTCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCCAGCTGT
329 329	Qy	5 ThrAspThrPheGliSerMetDroAspProGliGlvArgTvrThrPheGlvAlaSerCvs
1846 TTTCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTG 1905	Db	CTCCACTTCAACCACAGTGGCATCTGTGAGCTGCACTGCCCAGCCCTGGTCACCTACAAC
329 329	Qy	
		706 TGCCATGAGCAGTGTGCCGGCTGCACGGGCCCCAAGCACTCTGACTGCCTGGCCTGC 765

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US-08-356-786-1
              APPLICANT: Houston, ...
APPLICANT: Ring, David B.
TITLE OF INVENTION: Blosynthetic Binding Protein LU.
TITLE OF INVENTION: Marker
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Edmund R. Pitcher, Testa, Hurwitz, & ADDRESSE: Demund R. Pitcher, Pitc
                                                                                                                                                                                                                                                             Sequence 1, Application Patent No. 5877305 GENERAL INFORMATION: APPLICANT: Huston, J
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DB:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,82
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REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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LOCATION: 1..3768
OTHER INFORMATION:
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GlnArgAsnProGlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLys 194
                                                                         GlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIle
                                                                                                                                            GTGCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCCTCCCCAGGA
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35	2626 GAGTACCATGCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTC 2685	Db	_
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25	2566 CCCAACCATGTCAAAATTACAGACTTCGGGCTGGCTGGCT	Db	
w.	329 329	Qy	
55	2506 CTGGAGGATGTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGT 2565	Db.	
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5	2446 CGCCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTAC 2505	Db	
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'n	2386 CTGGTGACACAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAAACCGCGGA 2445	Db	*
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5	2326 GGTGTGGGCTCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAG 2385	рь	
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5	2146 AAAGAGACGGAGCTGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTAC 2205	Db	
•	329 329	Qy	
ū	2086 CTGGTGGAGCCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTG 2145	Db	
_	329 329	Qy	
5	2026 AAGCGACGGCAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAG 2085	Db	
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5	1966 TCTGCGGTGGTTGGCATTCTGCTGGTCGTGGTCTTTGGGGGTGGTCTTTGGGATCCTCATC 2025	Db	
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ThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValPro 546
                                                   AlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSer 527
                                                                                                                                      GlyLysAsnGlyValValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGlu
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                                          GCCTTCGACAACCTCTATTACTGGGACCAGGACCCACCAGAGCGGGGGGGCTCCACCCAGC
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Best Local Similarity:
                                                                                                                                                                                                                                             DB:
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                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application Patent No. 5976546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION UMBER: US/09/146
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: W. Hongyu
APPLICANT: W. Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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 236
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INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2385 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                              56 TTGCCCCCCGGAGCCGCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTC
                                                                                                                                                                            TOPOLOGY: linear
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ASPIleGlnGluValGlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValPro
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Conservative:
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Indels:
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414			GGGG 1308		tGly 385 : 1740	::: CCAG 1189	rGlu 371			gSer 341 GAGG 107	CAGC 101	329		SO C		м м м	м м м м	w w m w N		0 W B W B N 7 N			4 A 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	W W W W W W W W W W W W			у w m w m х z х z х m х л л л л г г	9 4 8 4 8 4 7 8 7 8 6 8 5 8 5 6 8		9 9 8 9 8 2 7 2 7 2 6 2 5 2 5 1 4 1 4 1	
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	655 2295	laThrGlnIleIleThrPheGluSerPheLy 	SCysProProThrProGluThrSerCysAlaThro	635 2236	Qy Db
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	615 2175	hrargLeuGluLeuTyrLysGlnGlyLeuar 	eAspLeuGlnGluProThrCysLeuGlnThr 	595 2116	Qу
	595 2115	stAsnGluThrValGluValIleSerGluMetPh 	nLeuSerArgAspThrAlaAlaGluM	2056	Qy Db
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	1944		OSerThrPhe	526 1885	Оy
	526 1884	InAspProProGluArgGlyAlaProPr :: GTTTCCAGATGAGGAGGGCGCATGCCAGCC	OAlaPheAspAsnLeuTyrTyrTrpAspGln.:: :: :: :: TGACCTCTCCTACATGCCCATCTGGAAG'	507 1828	Оy
	507 1827	TGCGTGGCCCGCTGCCCCAGCGGTGTGAAACC	AlaAlapro-GlnProHispro	495 1768	Qy Db
	494 1767	ProGlnGlyGly	ValGluAsnProGluTyrLeuThr	483 1708	Qу Дъ
	482 1707	LysaspValPheAlaPheGlyGlyAla ::: :: argccaggcacrgrrrgccgrgccacccrga	ACTGCAGGGGCTCCCCAGGGAGTATGTGAA	474 1648	Qy Db
•	473 1647	-SerProGlyLysAsnGlyValVal	ThrLeu	464 1588	Qу
	463 1587	gProAlaGlyAlaThrLeuGluArgAlaLys ccGAGGGCACTGCTGGGGTCCAGGGCCCAC	ProArgGluGlyProLeuProAlaAlaArgProA	444 1543	Db Oy
	443 1542	AGGACGAGTGTGGGGCGAGGGCCTGGCCTG	ValAsnGlnProAspValArgProGln::: :::	432 1486	Оy
	431 1485	laProLeuThrCysSerProGlaProGluTyr 	CCTCTGCTTCGTGCACACGTGCCCTGGC	415 1429	Qy Db
	1428	 GTGGACTGGCCCTCATCCACCATAACACCCA	GGGCTGCGCTCACTG	1369	Db

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US-09-821-883-2 (1-690) x US-08-579-823A-3 (1-2385)
                                                                                                                                                                                                                                                                                          Query Match:
DB:
                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                       US-08-579-823A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
TYPE: nucleic acid
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APPLICANT: Ruegg, Curt
APPLICANT: Wu, Hongyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01
FILING DATE: 03-DEC-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Judge, Linda REGISTRATION NUMBER:
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350 Cambridge Ave. Suite 250
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Sequence 3, Application US/09344195 Patent No. 6210662
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; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-C
; SEQUENCE DESCRIPTION: SEQ ID
US-09-344-195-3
                                                                                                                                                                                                                                                                                          US-09-821-883-2 (1-690) x US-09-344-195-3 (1-2385)
                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEPAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/09/146,283
FILING DATE: 03-SEPT-198
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Dehlinger & Associates
                                                                                                                                      ProAlaSerProGluThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnVal 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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                                                                 GATATCCAGGAGGTGCAGGGCTACGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCCA
                 AspīleGlnGluValGlnGlyTyrValLeuIleAlaHisAsnGlnValAryGlnValPro 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 350 Cambridge Ave. Suite 250 CITY: Palo Alto
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64.59%
62.18%
60.40%
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Q ID NO: 3:
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Matches:
Conservative:
Mismatches:
Indels:
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1368	GCCTACTCGCTGACCCTGCAAGGG	DЬ
408	ArgTyrSerGl	Qy
1308	1250 GCATG-GCCGGACAGCCTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGG 1	Db
402	laAlaLysGlyLeuGlnSerLeuProThrHisAspProSerPr	Qy
1249	1190 CCAGAGCAGCTCCAAGTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCA 1	뭥
385	1PheaspGlyAspLeuGlyMetGly	Qy
1189	GAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAG	g
371	uGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGlu	Q
1132	ATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTG	В
351	erSerThrArgSerGlyGlyGlyAspLeu	Qγ
1072	CCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGG	D
341	GlyAlaGlyGlyMetValHisHisArgHisArgSer	Qy
1015	AACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGC	B
329	329	Qy
		B
329	alThrAlaCysProTyrAsnTyrLeuSerThrAspValGlySer	γo
895	36 ACAGACACGTTTGAGTCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCCAGCTGT	Đ
314	hrAspThrPheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCys	δ
835 .	776 CTCCACTTCAACCACAGTGGCATCTGTGAGCTGCACTGCCCAGCCCTGGTCACCTACAAC (В
294	isPheAsnHisSerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsn	γ
775	716 TGCCATGAGCAGTGTGCTGCCGGCTGCACGGCCCCAAGCACTCTGACTGCCTGGCCTGC	В
274	5 CysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCys	Ş
715	656 ACGCGCACTGTCTGTGCCGGTGGCTGTGCCAGGGGGCCACTGCCACTGACTG	Ф
254	hrArgThrValCysAlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCys	γo
23 4 655	215 SerProMetCysLysGlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeu :	B 5
595	36 AACAACCAGCTGGCTCTCACACTGATAGACACCAACCGCTCTCGGGCCTGCCACCCCTGT	B
214	5 AsnAsnGlnLeuAlaLeuThrLeuTleAspThrAsnArgSerArgAlaCysHisProCys	9
535	76 CAGCGGAACCCCCAGCTCTGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAG	B
194	5 GlnArgAsnProGlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLys	8
475	6 GGCCTGCGGGAGCTGCAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATC	Db
174	55 GlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIle	Ş
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σ	35 ValLeuAspAsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSerProGly	Ş
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134	uGlnArgLeuArgIleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAla	οy

	٠	GTGAGACCGGCCAGATGAGGCT 2377	2356	Дb
		uGlyAlaProProProAla 682	675	Qy
	2355	AGG	2296	Db
	675	GluAsnLeuLysAspPheLeuLeuValIleProPheAspCysTrpGlunroValG	655	Qy
	N - 0	CTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAA	ن ن	₽ 4g
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	635 2235	gClySerLeuThrLysLeuLysGlyProLeuThrMetAlaSerHisTyrLysGlnHi 	615 2176	qa Vo
	2175	GACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGC	2116	Db
	615	pLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyL	595	Qγ
	2115	CCTGAGTAGAGACACTGCTGAGAGTGAATGAATGAAACAGTAGAAGTCATCTCAGAAATGTT	2056	Db
	595	LeuSerArgAspThrAlaAlaGluMetAsnGluThrValGluValIleSerGluMe	575	· Qy
	2055	CCCCAGCACACAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAA	1996	Дb
	575	ProSerThrGlnProTrpGluHisValAsnAlaIleGlnGluAlaArgArgLeuLe	555	Qy
٠.	1995	GAGAGAGCCAGCCCTCTGACGTCCCTCGAGGCACCCGCCCGCTCGCCCAG	1945	Дb
-	ទ ទ	luAsnProGluTyrLeuGlyLeuAspValProAlaAlaAlaProAlaArgSerPro	535	Qy
	1944	TTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGATGACAAGGGCTGCCCCGCCGA	1885	Db
	535	oSerThrPheLysGlyThrPtoThrAl	526	γo
	1884	GACCTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAGGGGGGATGCCAGC		뫄
	526	TyrTyrTrpAspGlnAspProProGluArgGlyAl	507	Qγ
-	1827	 	1768	: 당
	507	AlaAlaPro-GlnProHisProProProAlaPheSerPr	495	Qy
	1767	TGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAGGCTGACCAGTGTGTG	1708	ДЬ
	494	oGluTyrLeuThrproGlnGl	483	νο
	1707	ACTECAGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGTTTGCCGTGCCACCCTGA	1648	Дb
	482	ysAs	474	Qy
	1647	CCAGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGCGTGGAGGAATGCCGAGT	1588	ďď
	473	uSerProGlyLysAsnGlyValVal	464	Qy
	1587	ACCAGCTGTGCGCCCGAGGGCACTGCTGGGGTCCAG	1543	Db
	463 .	roArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArgAl	444	Оу
	1542	CACACTGCCAACCGGCCAGAGGACGAGTGTGTGGGCGAGG	1486	ДĎ
	443	\snGlnProAspVal	432	Qγ
	1485	CCTCTGCTTCGTGCACACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGC	1429	Db
	431	yTyrValAlaProLeuThrCysSerPro	415	Qy
	1428	GGGGCTGCGCTCACTGAGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCA	1369	ДĎ

RESULT 11 US-08-229-515A-14

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DB:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: SARKAR, FAZLUL H

TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN

TITLE OF INVENTION: NEOPLASTIC DISEASE

NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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CITY: Atlanta
STATE: Georgia
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           TyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGlyTyr 102
                                                                                                           GlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThrHisLeu
                                                                                                                                                             CAAGTGTGTACCGGCACAGACATGAAGTTGCGGCTCCCTGCCAGTCGTGAGACCCACCTG
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Matches:
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                                                                                                                                                                        GGGGACCCCTCCTCCGGCATTGCTCCGCTGAGGCCTGAGCAGCTCCAAGTGTTCGAAACC
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3;	CCCTACGGCTGCCTTCTGGACCATGTCCGAGAACACCGAGGTCGCCTAGGCTCCCCAGGAC 2	3:	GTGTCCCGCCTCCTGGGCATCTGCCTGACATCCACAGTACAGCTGGTGACACAGCTTATG 2	3:	AAAGCCAACAAAGAAATTCTAGATGAAGCGTATGTGATGGCTGGTGTGGGTTCTCCGTAT 2	3	GATGGGGAGAATGTGAAAATCCCCGTGGCTATCAAGGTGTTGAGAGAAAACACATCTCCT 2	3	AAGGTGAAGGTGCTTGGATCAGGAGCTTTTGGCACTGTCTACAAGGGCATCTGGATCCCA 2	3	CCCAGCGGAGCAATGCCCAACCAGGCTCAGATGCGGATCCTAAAAGAGACGGAGCTAAGG 2	3	ATCCGGAAGTATACGATGCGTAGGCTGCTGCAGGAAACTGAGTTAGTGGAGCCGCTGACG 2	3	CTGCTGTTCCTGATCTTAGTGGTGGTCGTTGGAATCCTAATCAAACGAAGGAGACAGAAG 2	3	TGCCCAGCAGAGCAGAGCCAGCCCGGTGACATTCATCATTGCAACTGTAGAGGGCGTC 2	3	ATATECCAGCCETECCCCATCAACTECACCCACTCCTETETEGATCTEGATGAACGAEGC 1	3	AGTGGTGTGAAACCGGACCTCTCCTACATGCCCATCTGGAAGTACCCGGATGAGGAGGGC 1	3	GATCAGTGTGCAGCCTGCGCCCACTACAAGGACTCGTCCTCCTGTGTGGCTCGCTGCCCC 1	3	CCGTGTCACCCCGAGTGTCAGCCTCAAAACAGCTCAGAGACCTGCTTTGGATCGGAGGCT 1	3	GAGGAGTGCCGAGTATGGAAGGGGCTCCCCCGGGAGTATGTGAGTGA	3	GGGCCAGGGCCCACCCAGTGTGTCAACTGCAGTCATTTCCTTCGGGGCCCAGGAGTGTGTG 1	3	GACTTGTGCGTCTCGAGCGGCTTGGTCTGTAACTCACTGTGTGCCCACGGGCACTGCTGG 1	3	GACCAGCTCTTCCGGAACCCCACATCAGGCCCTGCTCCACAGTGGGAACCGGCCGG	3	AGTGGATTGGCTCTGATTCACCGCAACGCCCATCTCTGCTTTGTACACACTGTACCTTGG 1
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453 3514	434 GlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAlaArg	Qу Db 3		
433 3454	414 SerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrValAsn 	Qy 3		
413 3394	394 ProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeuPro 4	Qy Db 3		
393 3334	374 GlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSerLeu 	Qу Db 3	. –	
373 3274	354 GlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGlyAla :	Qy Db 3		
353 3214	334 MetValHishisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThrLeu :	Qy Db 3		
333 3154	330	Qy Db 3		
3094	035 AGTACCTTCTACCGTTCACTGCTGGAAGATGACATGGGTGACCTGGTAGACGCTGAA	Db 3		
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3034	975 GACCCCCAGCGTTTTGTGGTCATCCAGAACGAGGACTTGGGCCCATCCAGCCCCATGGAC	Db 2		
329	329	Qy		
2974	15 GACTCTGAATGTCGCCCGAGATTCCGGGAGTTGGTGTCAGAATTTTCACGTATGGCGAGG	8		
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2854	2795 CCTTACGATGGAATCCCAGCCCGGGAGATCCCCTGATTTGCTGGAGAAGGGAGAACGCCTA	Db 2		
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279,4	2735 CAGAGTGATGTGGAGCTATGGAGTGACTGTGTGGGAGCTGATGACTTTTGGGGCCAAA	Db 2	_	
329	329	Qy		
2734	75 GGCAAGGTGCCCATCAAATGGATGGCATTGGAATCTATTCTCAGACGCCGGTTCACCCAT	2		
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2674	ATGCAGATGGG	Db 2		
329	329	Qy		
2614	TCAAGATT	Db 2		
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2554	2495 CTGCTCAACTGGTGTGTTCAGATTGCCAAGGGGATGAGCTACCTGGAGGACGTGCGGCTT ;	Db 2		•

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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
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MEDIUM TYPE: Floppy disk
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NAME: PERRYMAN, DAVID G
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
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STATE: Georgia
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SYSTEM: PC-DOS/MS-DOS
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                                                            ACAGCTGAGGACGGAACACAGCGTTGTGAGAAATGCAGCAAGCCCTGTGCTCGAGTGTGC
                                                                                                                                                                     TyrLeuSerThrAspValGlySer-----
                                                                                                                                                                                                                                                       ProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysProTyrAsn
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                                                                                                                                               TACCTGTCTACGGAAGTGGGATCCTGCACTCTGGTGTGTCCCCCGAATAACCAAGAGGTC
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ACAGCCCATAGAAGGCACCGCAGCTCCTCCACCAGGAGTGGAGGTGGTGAGCTGACACTG 3214		AGTACCTTCTACCGTTCACTGCTGGAAGATGATGACATGGGTGACCTGGTAGACGCTGAA 3094	GACCCCCAGCGTTTTGTGGTCATCCAGAACGAGGACTTGGGCCCCATCCAGCCCCATGGAC 3034	GACTCTGAATGTCGCCCGAGATTCCGGGAGTTGGTGTCAGAATTTTCACGTATGGCGAGG 2974		329	CCTTACGATGGAATCCCAGCCCGGGAGATCCCCTGATTTGCTGGAGAAGGGAAACGCCTA 285	CAGAGTGATGTGTGGAGCTATGGAGTGACTGTGTGGGAGCTGATGACTTTTGGGGCCAAA 2794	329	GGCAAGGTGCCCATCAAATGGATGGCATTGGAATCTATTCTCAGACGCCGGTTCACCCAT 2734	ACAGATTTCGGGCTGGCTGGCTGCTGGACATTGATGAGACAGAGTACCATGCAGATGGG 2574	329	GTACACAGGGACCTGGCTGCCCGGAATGTGCTAGTCAAGAGTCCCAACCAGGTCAAGATT 2614	CTGCTCAACTGGTGTGTTCAGATTGCCAAGGGGATGAGCTACCTGGAGGAČGTGCGGCTT 2554	329	CCCTACGGCTGCCTTCTGGACCATGTCCGAGAACACCGAGGTCGCCTAGGCTCCCAGGAC 2494		329 GTGTCCCGCCTCCTGGGCATCTGCCTGACATCCACAGTACAGCTGGTGACACAGCTTATG 2434	AAAGCCAACAAAGAAATTCTAGATGAAGCGTATGTGATGGCTGGTGTGGGTTCTCCGTAT 2374	GATGGGGAGAATGTGAAAATCCCCGTGGCTATCAAGGTGTTGAGAGAAAAACATCTCCT 2314		AAGGTGAAGGTGCTTGGATCAGGAGCTTTTGGCACTGTCTACAAGGGCATCTGGATCCCA 2254	329	

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Sequence 2, Application US/08422108 Patent No. 6015567
                                                                                                                                                                                     Genentech, Inc.

CITY: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                         SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,108
FILING DATE: 14-Apr-1995
                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: 08/3 FILING DATE: 13-DEC-1994
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Best Local Similarity:
Query Match:
DB:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 07/3
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: Sing
TOPOLOGY: Linear
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GlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCysAla
                                              SerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCysAla
                                                                                                          ThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGly
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Matches:
Conservative:
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US-08-422-108-2

GENERAL INFORMATION: APPLICANT: Hudzia

APPLICANT: Shepard, APPLICANT: Ullrich, TITLE OF INVENTION:

Shepard, Ullrich,

NUMBER OF SEQUENCES:

COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc

CLASSIFICATION: 435 PRIOR APPLICATION DATA:

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AGGGTC Hisval 564

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Db 1554 GUGCUGGAGAAUGCCGAGGAGUACUGCCCAGGAGUAUGGGAAUGCCAGGAAGUAUGGGAAUGCCAGGAAGUAUGGCAAGGAAUAUGCCAAGGAAUACUAUGCCAAGGAAUACUAUGCCAAGGAAUACUAUGCCAAGGAAUACCCAAGGAAUACCCAAGGAAUACCCAAGGAAUACCCAAGGAAUACCCAAGGAAUACCCAAGGAAUACCCAAGGAAUACCCAAGGAAUACCCAAGGAAUACCCAAGGACAACAAGGACAACAAGGACAACAACAACAAC	495 AlaAlaProGInProHisProPro	ProAspValargProGlnProProSerProArgGluGlyProLeuProAlaAlaArgPro ::	368 AlaProSerGluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAla 387 1015 AAUAUCCAGGAGUUUGCUGCCAAGAAGAUCUUUGGGAGCCUGGCAUUU 1065 388 LysGlyLeuGlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAsp 407 1065	261 AlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAspHisSer 280 261 AlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAspHisSer 280 261 AlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAspHisSer 280 261 GCGGCUGCACGGGCCCAAGCACCUCUGACCCUGGCCCUGCCCCCCCC
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	FION NUMBER: 08/355460 ATE: 13-DEC-1994 LICATION DATA: FION NUMBER: 08/048346 ATE: 15-APR-1993 LICATION DATA: FION NUMBER: 07/354319 AATE: 19-MAX-1989 AGENT INFORMATION: Lee, Wendy M ATION NUMBER: 00,000 TON NUMBER: 554C2D1 STON NUMBER: 554C2D1 STON NUMBER: 554C2D1 STON STON INFORMATION: LEE: 415/252-1994 15/371-7168 FOR SEO ID NO: 2: CHARACTERISTICS:	OBO DEADABLE FORM: EADABLE FORM: LEM PC compatible SYSTEM: PC DOS/MS DOS WinPatin (Genentech) PLICATION DATA: ION NUMBER: US/08/422,734 ATE: CATION DATA: ION NUMBER: 08/422108 ION NUMBER: 08/422108 ION NUMBER: 108/422108	2-734-2 2-734-2 No. 6333169 NL INFORMATION: LICANT: Hudziak, Rober JCANT: Shepard, H. Mi JCANT: Sepondore, J. Mi REET: 460 point San B REET: 460 point San B REET: South San Francis ATE: Callfornia JUNTRY: USA	nGluAl nGluAl lGuva lGluva lGuva lGuva lGuva lGuva lGuva lGuva lGugga lGugga lGugga lGugga lGugga lGugga lGugga lGugga lGugga
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; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
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           SerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCysAla
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roLeuLeuLeuAlaArgA] cccrccrccrgccAGGGC	US-09-821-883-2 (1-690) x US-09-146-283-1 (1-1588)	20.59% Indels: 2 Gaps:	: 770.00 Matches: 257 nt Similarity: 42.14% Conservative: 54 Local Similarity: 34.82% Mismatches: 159	I.ength.	; LIBRARY: prostate carcinoma LnCaP.FGC; PBMC US-09-146-283-1	; INDIVIDUAL ISOLATE: Prostatic acid phosphatase-GM-CSF; INDIVIDUAL ISOLATE: fusion gene; Fig. 1; IMMEDIATE SOURCE:	ORIGINAL SUNCE:	E PE	nucleic acid DNESS: doub Y: linear	rg	TELEPHONE: 650-324-0880 ; TELEFAX: 650-324-0960 ; INFORMATION FOR SEQ ID NO: 1:	REGISTRATION NUMBER: 42,702 REFERENCE/DOCKET NUMBER: 7636-0010.21 TELECOMMUNICATION INFORMATION:	₩ 7	3 8 2	COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CIBERT ADDITARTON DATA	; COUNTRY: USA ; ZIP: 94306 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk	- >	SEQUENCES: DENCE ADDRES EE: Dehling	Wu, Hongyu NVENTION: Immun	; APPLICANT: Ruegg, Curtis L.	, sequence 1, application 05/09146263 ; Patent No. 5976946 . GENERAL THEORYTON.	283-1	1770 GCCCAUCUGGAAGUUUCCAGAUGAGGAGGGCGCAUGCCAGCCU	665 eProPheAspCysTrpGluProValGlnGluGlyAlaProProPro 680	Qy 645 aThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValI1 665 ::: :: :: Db 1740 CAGC	Db 1686 GUGUGUGGCCUGUGCCCACUAUAAGGACCCUCCCUUCUGGCGUGGCCCGCUGCCC 1739
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353 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 372	603GGCCAGGACCTTTTT 623	GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr ::::		SprCvsValThrAlaCvsDroTvrAspTvrI.puSprThrAspValGlvSprGlvAlaGlv	293 TyrasnThraspThrPheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAla 312 293 TyrasnThrAspThrPheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAla 312 513 CTTGAGAGTGAACTTTGAAATCAGAAGTAGAAGAAGAGGTTGCAC 550	CTATACCTGCCTTTCAGG	420 NOCKAGCCCAICCCGGIOCACACAGIICCICIIICIGAAGAICAGIIC 4/3	spCysCysHisGluGlnCysAlaAlaGlyCys-ThrGlyProLysHisSerAspCysLeu	ATCTGGAATCCTATCCTACTC	erLeuThrArgThrValCvsÅlaGlvGlvCvsAlaArgCvsLvsGlvProLeuProThrA	213 roCysSerProMetCysLysGlySerArgCysTrpGlyGluSerSerGluAspCysGlnS 233	312 GAACAGGTTTATATTCGAAGCACAGACGTTGACCGGACTTTGATGAGTGCTATGACAAAC 371	ARGAGATATAGAAAATTCTTGAATGAGTCCTATAAACAT	ArgAsnProGlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsn	156 LeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGln 175 :::	141ProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGly 155	:::	119	101 GlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArgIle 120	119 119	81 LeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGln 100		119 119	41 SerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThr 60	75 CTGCTTTTTTTCTGGCTAGACCGAAGTGTACTAGCCAAGGAGTTG	10:10:10:00:00:00:00:00:00:00:00:00:00:0

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628 1418	LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet	609 1359
608 1358	GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 	589 1299
588 1298	GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal	569 1239
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	CAATGAAATCCTCAATCACATGAAGAGAGCAACTCAGATACCAAGCTACAAAAAACT	ō
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425 803	hrValProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCys	409 744
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

Minimum DB seq length: 0
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ValProLeuGlnArgLeuArgIleValArgGlyThrGlnLeuPheGluAspAsnTyrAla 132
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D
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/lab_host="DHIOB (phage-resistant)"
/note="forgan: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
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AF318349.1 G
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                           Huang,Y., Zhou,X.M., Wan,D.F. and Gu,J.R. Direct Submission
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Novel human cDNA
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SPLQRYSEDPTWPLPSETDGYVAPLTCSPQPEXYUNQPDVRPQPESPREGPLPAARPAG
ATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPGGGAALSPTLLLPSAQPSTTSIT
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/protein_id="AAL55856.1"
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/db_xref="GI:18027790"
/translation="MALESILERRETHQSDVWSYGVTVWELMTFGAKDYDGIPAREIP
DLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ
NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento
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Fax: 319 335 9565
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Seq primer: M13 Reverse.
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constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the
                                                                                                                                           /Glone="UI-E-EO1 alb-p-15-0-UI"
/Glone_lib="UI-E-EO1"
/Clone_lib="UI-E-EO1"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (pharmacia) with a
modified polylinker; Site_1: EOR I; Site_2: Not I;
UI-E-EO1 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
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/db_xref="taxon:9606"
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DKFZp686P06148 5', mRN
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a 226 c 188 g 108 t 1 others
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Eutheria;
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           LysHisSerAspCysLeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLeuHis
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AAGCACTCTGACTGCCTGGCCTGCCTCCACTTCAACCACAGTGGCATCTGTGAGCTGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone (DKFZp686P06148) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duesterhoeft, A., Lauber, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpubl
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ublished (1999)
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cDNA-collection"
187 c    156 g    110 t    1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
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/clone_lib="686 (synonym: hlcc3)"
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/db_xref="taxon:9606"
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IMAGE:6485621 5', mRNA sequence.
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BQ958632 GI:22374110
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM14027 row: 1 column: 06
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Location/Qualifiers
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
312 c 249 g 179 t
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/clone="IMAGE:6485621"
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                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deno
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM11733 row: 1 column: 20
High quality sequence stop: 801.
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603236977F1 NCI_CGAP_Mam3
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National Institutes of Health, Mammalian
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
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/dev_stage="10 months"
/lab_host="DH10B"
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            LeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLeuHisCysProAlaLeuVal
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High quality sequence start: 12
High quality sequence stop: 612.
Location/Qualifiers
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Seq.primer: puc 18 forward
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This sequence was derived from the FAPESP/LICR Human Cancer
Project. This entry can be seen in the following URL.
Project. This entry can be seen in the following URL.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer R
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/dev_stage="Adult"
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http://image.llnl.gov
plate: LLAMI1090 row: b column:
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Den-
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information ca
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National Institutes of Health, Mammalian Gene Collection
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/lab_host="DH10B"
/nofe="^~~-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5032238"
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                                                                                                   52 Eoeun-dong Yuseong-gu,
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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K-EST0070099 S22SNU16
                                                                                                                                                    Contact: Kim YS
Genome Research Center
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                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 491)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.
                                                                          Email: yongsung@mail.kribb.re.kr
Plate: 3 row: A column: 11
                                                                                                                           Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                              Unpublished
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Location/Qualifiers
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 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNU16-3-A11"
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/cell_line="SNU-16"
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                                                                                         CysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnProProSerPro
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                                                                                                                                                                                                                                    TCTCCACTGGCTCCCTCCGAAGGGGTTGGCTCCGATGTGTTTGATGGTGACCTGGCAGTG
LeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGlyAlaValGlu
                                                                            TGCAGCCCCAGCCCGAGTATGTGAACCAGCCAGAGGTTCGGCCTCAGTCTCCCTTGACC
                                                                                                                                AGTGAGGATCCCACATTACCTCTGCCCCCCGAGACTGATGGCTACGTTGCTCCCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11856 row: o column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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Eukaryota; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
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/strain="129,C57BL/6J,FVB/N"
/db_xref="texon:10090"
/clone="IMAGE:5337435"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oilgo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics
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/lab_host="DH10B"
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AU123871
                                                                                                      Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end on
Research Institute; cDNA library constr
Virology, Institute of Medical Science,
                                                                                                                                                                                                                Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                           HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S. Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzu,Y., Sugano,S., Isogai,T.)
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Nakamura,Y., Nishikawa,T., Nagai,T.,
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                                                                                                                                                                                                                                                                                Genomics Laboratory
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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cal Science, University of Tokyo, and
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i,T., Suzuki,Y., Suga
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                                                                            uq93002.y1 NCI_CGAP_Mam10 Mus musculus cDNA clone IMAGE:2938635 5' similar to gb:M11730 ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (HUMAN); mRNA sequence.
AM701942
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 609)
                                   Mus musculus
                                                         EST
                                              house mouse
                                                                   AW701942.1 GI:7586086
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/clone_11b="NYT2RM2"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA fiprecursor cells"
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Contact: Robert Strausberg, Ph.D.
Contact: Copapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Jeff
Gilbert Smith, Ph.D., William Muller, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
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/lab_host="DH10B (phage-resistant)"
/note="Organ: mammary gland; Vector: PT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled mammary gland tumors with a Not I - oligo(dT)
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/db_xref="taxon:10090"
/clone="IMAGE:2938635"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 621)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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BG283493
BG283493.1 GI:13033480
EST.
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM10416 row: d column: 21
High quality sequence stop: 602.
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Tissue Procurement: DCTD/DTP
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                                                                                                         /tissue_type="adenocarcinoma, cell line"
/lab_host="pHiOB (phage-resistant)"
/note="organ: prostate; Vector: pcMV-SPORT6; Site_1: Not
Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NHH_MGC Library."
a 207 c 178 g 104 t . 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:4519652"
/clone_lib="NIH_MGC_91"
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391 GlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal
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                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I (bases 1 to 887)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
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                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAN13589 row: 1 column: 02
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                                                                               quality sequence stop:
                                      Location/Qualifiers
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/organism="Homo sapiens'
/db_xref="taxon:9606"
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Query Match:
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291 c
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Database: N_Geneseq_101002:* 1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:* 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:* 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:* 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:* 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:* 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:* 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:* 8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:* 9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:* 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:* 11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:* 12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:* 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:* 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:* 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 25: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 26: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 27: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 28: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 29: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*	Command line parameters: -MODEL-frame+_p2n.model -DEV-xlp -Q-/cgn2_1/USPTO_spool/USO9921883/runat_28042003_104748_14558/app_query.fasta_1 -Q-/cgn2_1/USPTO_spool/USO9921883/runat_28042003_104748_14558/app_query.fasta_1 -DB-N_Geneseq_101002 -QFMT-fastap -SUPFIX-p2n.rng -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-biosum62 -TRAMS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000 -USER-USO9821883_CGGN_1_1_396_Grunat_28042003_104748_14558 -NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPOP-10 -YGAPOP-5 -DELEXT-7	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Total number of hits satisfying chosen parameters: 4370478	Searched: 2185239 seqs, 1125999159 residues	Scoring table: BLOSUM62 X9apop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0	Title: US-09-821-883-2 Perfect score: 3739 Sequence: 1 MRAAPLILARAASLSLGFLFEPVQEGAPPPPAAAHHHHHH 690	Run on: May 7, 2003, 22:19:33 ; Search time 1592 Seconds (without alignments) 976.055 Million cell updates/sec	OM protein - nucleic search, using frame_plus_p2n model	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AAD21565 standard; DNA; 2070 BP

28-JAN-2002 (first entry)

Human HER500-hGM-CSF fusion DNA construct.

RESULT 1
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XX AAD2
XX Huma
XX Immu
KW Immu
KW Immu
KW Immu
KW dend
KW dend
KW dend
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KW dend
KW HERKW HERKW HERS Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendrittic cell; colon cancer; breast carcinoma; ovarian cancer pape protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF; HER-2 protein; granulocyte-macrophage colony stimulating factor; HER500-hGM-CSF fusion DNA; ds.

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                          CC The invention relates to immunostimulatory fusion proteins (IFP) and CC nucleic acid molecules encoding such proteins. The IFPs comprise a CC polypeptide antigen component and an immunostimulatory component derived CC from the intracellular domain of HER-2 protein which is effective to CC elicit a protective dendritic cell (DC) induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells CC are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer CC associated with a particularly antigen. The present sequence is HER500 hGM-CSF fusion DNA construct which comprises DNA molecules encoding CC human PAP signal sequence, mature PAP protein, an Ala Arg linker, human CC HER-2 signal sequence, mature HER-2 membrane distal, extracellular and CC intracellular domains, an Ala Ala linker, a mature human granulocyte- macrophage colony stimulating factor (GM-CSF) sequence and a CC c-terminal tag.
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                         SerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThr
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human GM-CSF sequence and a C-terminal tag"
/note= "CDS does not include stop codon"
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                Immunostimulatory fusion protein; IFP; antigen component; thérapy; immunostimulatory component; T-cell mediated immune response; DC; dendrittic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

3.17e-144 3473.50 94.42% 91.70% 92.90%

Conservative: Mismatches: Indels:

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                                                            are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 rGM-CSF fusion DNA construct which comprises DNA molecules encoding human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodominant octapeptide, HER-2 membrane distal intracellular domain, an Ala Ala linker, a mature.
                                                                                                                                                                        The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells
Sequence
                                                                                                                                                                                                                                                                                                                   An immunostimulatory fusion protein comprising the intracellular domain of HER-2 and an antigen elicits an immune response to the antigen and is useful for the treatment of associated cancer associated -
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                                                                                                                                                                                                                                                                                    immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 fusion DNA construct which comprises DNA molecules encoding human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 membrane distal extracellular and intracellular domains and a communication of the color of the
                                                                                                                                                                                                                                                                                                                                                                                nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HBR-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or emporantimental 3-13
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protein; Ala Arg linker; membrane distal extracellular domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carchnoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; OVA; HER-2 protein; ovalbumin-derived octapeptide; HER500 fusion DNA; d
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  30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                      /product= "Human HER500 fusion protein construcomprising human PAP signal sequence, mature F protein, an Ala Arg linker, human HER-2 signal
                                                                                                                                                                                                                                          sequence, mature HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodominant octapeptide, HER-2 membrane distal intracellular domain and a C-terminal tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HEB500 fusion DNA construct which comprises DNA molecules encoding human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 membrane distal extracellular domain, an Ala linker, an ovalbumin (OVA)-derived immunodominant octapeptide, HER-2 membrane distal intracellular domain and a C-terminal tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An immunostimulatory fusion protein comprising the intracellular of HER-2 and an antigen elicits an immune response to the antigen is useful for the treatment of associated cancer associated -
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Length:
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                       The Erb-B2 gene is one of the primary genes responsible for the transition of normal breast epithelial cells towards carcinoma in situ and the subsequent development of invasive and metastatic cancer. HPBF (see AAR7703-94), the Erb-B2 promoter binding protein, induces cell division on binding to the promoter. In a method for greater success in early identification and treatment of breast cancer, the initation step for Erb-B2 gene activity is identified. This method involves determining the presence of HPBF in a biopsy from the subject, where the presence of HPBF (relative to its absence in a normal control) indicates the presence of cancer and a decreased chance of long-term survival. Binding of HPBF to the promoter can be inhibited using antisense oligonucleotides or a non-genomic nucleic acid that binds to HPBF; these oligos can be expressed from retro virus or other gene therapy vectors.
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                                                                                                                                                                                                                                            Disclosure; Page 52-54; 69pp; English
                                                                                                                                                                                                                                                                                    New purified protein binding to the ERBB2 gene promoter - to cell proliferation, diagnostic of breast cancer, also related antibodies, nucleic acid, assays and methods for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Her-2/neu; Erb-B2; c-erbB-2; oncogene; DNA binding protein; HPBF; Erb-B2 promoter binding protein; tumour enhancer factor; breast cancer diagnosis; prognosis; antisense oligonucleotide; retro virus vector; gene therapy vector; ss.
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2185 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG 2244		1105 AACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGT 11	ם
329 329	Qy	329	δ
2125 GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGG 2184	Db		D
329 329	Qy	318 CysProTyrAsnTyrLeuSerThrAspValGlySer	δō
2065 GACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTG 2124	Db	985 TTTGAGTCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCC 1	D
329 329	Qy	298 PheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla 3	o
2005 GAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGAT 2064	ф	925 AACCACAGTGGCATCTGTGAGCTGCACAGCCCTGGTCACCTACAACACAGACACGGC 98	0 1
329 329	Оу	278 AsnHisSerGlvIleCvsGluLeuHisCvsProAlaLeuValThrTvrAsnThrAsnThr	٥
1945 CGCTGCCCCAGCGGTGTGAAACCTGACCTCCTACATGCCCATCTGGAAGTTTCCAGAT 2004	Db		ם ו
329 329	Qy	258 GlnCvsAlaAlaGlvCvsThrGlvProLvsHisSerAspCvsLenAlaCvsLenHisPhe 2	0
1885 CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTTCCTGCGTGGCC 1944	Db		, a
329 329	. Qy	238 VAlCvsAlaGlvClvcvsAlaArrrCvsIvsGlvDrnIenDrnThrasnCvsCvsBisGln 2	0
1825 CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA 1884	Db	745 TGTAAGGGCTGCCGCTGCGGGAGAGAGTTCTGAGGATTGTCAGAGGCCTGACGCGCACT	. ا
329 329	Qy	218 CysLysGlySerArqCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArqThr 2	0
1765 GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCCAGGGAGTATGTGAATGCCAGG 1824	מם		0
329 329	Qy	198 LeualaLeuThrLeuIleAspThrAsnArqSerArqAlaCvsHisProCvsSerProMet 2	٥
1705 CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG 1764	Db	625 CCCCAGCTCTGCTACCAGGACACGATTTTGTGGAAAGACTCTTCCACAAGAACAACCAG	
9		Oy 178 ProGlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheH1sLysAsnAsnGln 197	0
S CGGCCAGAGGACGAGTGTGGGCGAGGGCCTGGCCACCAGCTGTGCGCCCGAGGG		Db 565 GAGCTGCAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAAC 624	D
	2	Oy 158 GluLeuGlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsn 177	o
20		Db 505 AATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCCAGGAGGCCTGCGG 564	
85 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC	Db .	138 AsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArg 1	
329 329	Qy	יים	
1525 AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 1584	Db		.
329 329	Оу	118 LeuArgI eVa ArgG v™hrG nLeuDheG uAscAscn™vrA aLeuA aVa LeuAscn	0
1465 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGGCTGGGGCTGCGCTCACTG 1524	מם		D
329 329	Qy	98 GluValGlnGlvTvrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArg 1	0
1405 CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGGACGAATTCTGCACAAT 1464	ф	325 AACCTGGAACTCACCTACCTGCCCACCAATGCCAGCCTGTCCTTCCT	5
329 329	Qy	78 AsnLeuGluLeuThrTvrLeuProThrAsnAlaSerLeuSerPheLeuGlnAsnTleGln 9	0
1345 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 1404	Дb	265 CCCGAGACCCTGGACATGCTCCGCCACCTCTACCAGGGCTGCCAGGTGGTGCAGGGA	
329 329	Qy	7	0
1285 GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG	Db	Db 205 GGAGCCGCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGT 264	
329 329	. Qy	Oy 38 GlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSer 57	o
25 GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG	Db	::: GCTCCTCCTCGCCCTCTTGCCCCCC	ы
329 329 -	Qy	PheLeuLeuPhePheTrpLeuAspArgSerValLeuAlaLysG	0
1165 GCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCCAGTTACCAGT 1224	. Db	94 CGCGCCCTCCCAGCCGGGTCCAGCCGGAGCCATGGGGGCCGGAGCCGCAGTGAGCACCATG 1	
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Deletion of amino acids 1-731 of the encoded protein renders the CTG non-transforming. HER2 is a tyrosine kinase-type receptor. This sequence can be used in the cellular immunogen of the invention. The cellular immunogen of the invention. The cellular immunogen of the invention. The cellular cancer, comprises host cells transfected with a construct containing at least one transgene related to the proto-oncogene and driven by a strong promoter. The product of the transgene induces immunoreactivity to host self-determinants on the product of proto-oncogene. The cellular immunogens are used for protective vaccination against cancer (e.g. carcinoma of breast or colon, or various lymphomas) and for immunotherapy of cancer. Use of the immunogen eliminates the need to isolate recognition of a determinant defined by a cancer-specific mutation and generates a systemic (anti-metastatic) response.
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                                                                                          GlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSer
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                                                     CGGCCAGAGGACGAGTGTGTGGGCCAGGCCTGCCCACCAGCTGTGCGCCCGAGGG
                                                                                                          ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC
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                                                                                                                                                                                                                           The present sequence represents a cognate transgene (CTG) which is created non-tumourigenic by deletion of amino acids 1-731. The CTG is used in the course of the invention. The specification describes a cellular immunogen for immunizing a host against the effects of the product of a target proto-oncogene which is associated with a malignanacy. The cellular immunogen comprises allogenic cells transfected with transgene construct comprising a transgene cognate to target proto-oncogene and a strong promoter. The cellular immunogen is useful for vaccinating a host against cancer by inserting the transgene construct into the body of the host for the expression of the transgene. The method of the invention is designed to target mutation-driven non-self determinants. The cellular immunogens induce reactivity for self-determinants in the over expressed product of tumour associated and over expressed proto-oncogenes.
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			2185 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG 2244
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	CCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTG	, Db	GACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTG
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	3085 ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	Db	GAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCCACTCCTGTGTGGACCTGGAT
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	2965 GAGCGGCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT 3024	Db	1885 CCGGAGGCTGACCAGTGTGGGCCTGTGCCCACTATAAGGACCCTCCCT
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•	2845 TTCACCCACCAGAGTGATGTGGGGGTTATGGTGTGACTGTGTGGGGAGCTGATGACTTTT 2904	da	GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGGAGTATGTGAATGCCAGG
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~	2785 GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG 2844	. Db	1705 CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCCTTCGGGGCCAG 1764
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	2665 GTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAT 2724	. <u> </u>	1585 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC 1644
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	2605 TCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGAT 2664	Db	AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACC
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	2485 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCACCTGGTGACA 2544	da	CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAACTAGTTCTGCACAAT
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                                                                                                                                                                                                                                                                           kinase-type receptor, HER-2 cDNA.
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Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties

Disclosure; Page 57-63; 69pp; English

for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of gen transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host cells. The present The invention relates to synthetic theraputic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful sequence is human tyrosine kinase-type receptor, genes of gene ls (APCs), to

Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 other;

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329 329	Qy		58 GlnCvshlahlaGlvCvsThrGlvDroIvsHtsGorhsnCvsIonhlaCvsIonHtsDho 27
1885 CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCCTTCTGCGTGGCC 1944	рb		808 GTTTGGTTGATTGATTGATTGATGATGATGATGATGATGA
329 329	Qy		
1825 CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA I884	Db		
329 329	Qy		0
1765 GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCCTCCCCAGGGAGTATGTGAATGCCAGG 1824	Db		98 LeuAlaLeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMet 2

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                      GGGACACCTACGGCAGAGAACCCCAGAGTACCTGGGTCTGGACGTGCCA-----GTGTGA 3918
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GlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSer

-GGGCTCCTCCTCGCCCTCTTGCCCCCC

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04-DEC-2000;
11-JUN-2001;
                                                                                                                                                                                                                                                                                            receptor tyrosine kinase targeted agent for treating tumour by amplifying mRNA from tumour and non-malignant tissues using a primer pair that hybridises to epidermal growth factor receptor (EGER) and/or HER2-neu gene (I), quantitating and obtaining differential expression levels of amplified mRNA and comparing the differential expression levels and threshold levels for expression of (I). The method is useful for assessment of clinical treatment of a patient and as a diagnostic or prognostic tool for a range of cancers including breast, head and neck, lung, oesophageal and colorectal cancer. The present sequence is that of the human HER2-neu DNA sequence used in methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining chemotherapeutic regimen of receptor tyrosine kinase targeted agent for treating tumor by examining EGFR and/or HER2-neu mRNA amount in tumor cells, comparing it to predetermined threshold expression level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression level
                                                                                                                                                                                                                                                                   Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to determining the chemotherapeutic regimen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 124-125; 125pp; English.
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2365 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2424	. Db			•
329 329	Qy		329	< 1
2305 GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCCATC 2364	Db		1225 GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAAGCCTTGGCATTTTTGCCG	σ,
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2245 CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG 2304	Db		том с отметь и соловательно в соловым проводения по проводения по проводения по проводения по проводения по пр	,
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329 329	Qy			~
2125 GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGTCTTTGGGATCCTCATCAAGCGACGG 2184	Db			σ
329 329	Qy		318 CysProTyrAsnTyrLeuSerThrAspValGlySer 329	~
2065 GACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTG 2124	Db			σ,
329 329	Qy		PheGluSerMetProAsnProGluGlvArgTvrThrPheGlvAlaSerCvsValThrAla	<
2005 GAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGGACCTGGAT 2064	дд		AACCACAGTGGCATCTGTGAGCTGCACTGCCCAGGCCTGGTCACCTACAACACAGACACAG	۵,
329 329	Оу		AsaH1sSerG]vT]eOvsG]iiLeiiH1sOvsPrOA]aLeiiVa]ThrTvrAsaThrAsaThr	ς .
1945 CGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCCATCTGGAAGTTTCCAGAT 2004	Db		CAGTGTGCTGCCGGCTGCACGGGCCCCAAGCACTCTGACTGCCTGGCCTGCCCTCCACTTC	σ .
329 329	Qy		GInCvsAlaAlaGlvCvsThrGlvDroIvsH1sSprAspCvsIonAlaCvsIonH1sDho	<
1885 CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT	g _Q		GTCTGTGCCGGTGGCCCGCTGCAAGGGGCCACTGCCCACTGACTG	σ,
329 329	Qy		ValCvsAlaGlvGlvCvsAlaArgCvsLvsGlvProLeuProThrAspCvsAvsHisGlu	<
1825 CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA 1884	Db		TGTAAGGGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTGTCAGAACCCTGAACGCACT	۰ ،
329 329	Ωу		CvsLvsGlvSerArgCvsTrpGlvGluSerSerGluAspCvsGlnSerLenThrArgThr	<
1765 GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGG 1824	ф		CTGGCTCTCACACTGATAGACACCCACCGCTCTCGGGGCCTGCCACCCCTGTTCTCCGATG	σ,
329 329	Ωу		LeuAlaLeuThrLeuIleAspThrAspArgSerArgAlaCvsHisProCvsSerProMet	<
1705 CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG 1764	Db	: .	CCCCAGCTCTGCTACCAGGACACGATTTTGTGGAAAGGACATCTTCCACAAAGAACAACCAG	0 -
329 329	Qy	:	ProGlnLeuCvsTvrGlnAspThrTleLeuTrpLvsAspTleDheHisLvsAspAspGln	<
1645 CGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCGAGGG 1704	Дb		The second sec	o .
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1585 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC 1644	Дb			o 4
329 329	Qy			
1525 AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 1584	Db			J .
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329 329	, Oy		GliValGlnGlvTvrValIeiiTlealaHisassGlsValarcGlsValarcIeiiGlsiarc	ς
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1345 GTGTTTGAGACTCTGGAAGAGATCACAĢGTTACCTATACATCTCAGCATGGCCGGACAGC 1404	Db	• .		, ,
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1285 GAGAGCTTTGATGGGGACCCCAGCCTCCAACACTGCCCCGCTCCAGCCCAGAGCAGCTCCAA 1344	Db			Ö

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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and

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                                                          vention relates to detecting (M1) granulocyte (GC) active by detecting the level of expression of gene(s) (Gs) idd to analysis as given in the specification, and comparing pression level to an expression level in an unactivated
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                                                                        CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGGACGAATTCTGCACAAT 1464
                                                                                                                                 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 1404
                                                                                                                                                                                                                                                  GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG 128
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317 984 297 924 277 864 257

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804 237 744 684

217

624 177

Ş	329	3	329
В	1525	AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 1	1584
Ş	329	3:	329
В	1585	ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC 1	1644
δ	329	3:	329
ᄝ	1645	CGGCCAGAGGACGAGTGTGTGGGGCGAGGGCCTGGCCTG	1704
Ş	329	3;	329
망	1705	CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG 1	1764
Ş	329	3:	329
<u>р</u>	1765		1824
γQ	329	3:	329
망	1825	CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA 1	1884
γ	329	3:	329
망	1885	CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT	1944
δ	329	3:	329
В	1945	CGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCCATCTGGAAGTTTCCAGAT 20	2004
δ	329	3;	329
용	2005	GAGGAGGGCGCATGCCAGCCTTGCCCCCATCAACTGCACCCCACTCCTGTGTGGACCTGGAT 20	2064
οy	329	3;	329
Ъ	2065	GACAAGGGCTGCCCCGCCGAGCAGAGAGCCCAGCCCTCTGACGTCCATCGTCTCTGCGGTG 2:	2124
Qy	329	3	329
В	2125	GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGG 2:	2184
γ	329	3;	329
В	2185	CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG 2:	2244
Qγ	329	3;	329
В	2245	CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGGATCCTGAAAGAGACG 2:	2304
γQ	329	3	329
망	2305	GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATC 2:	2364
δ	329	3	329
В	2365	TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2	2424
QY	329	37	329
Вb	2425	ACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC 24	2484
δĀ	329	35	329
B	2485	TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA 2:	2544
δ	329	3:	29
В	2545	CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGC 20	604
Q	329	31	29

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ŏ	GlyValValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThr 49	471	Qy
84		25	Db
0	aAlaArqProAlaGlyAlaThrLeuGluArqAlaLysThrLeuSerPrcGlyLysAsn 47	451	0γ
524		3565	Db
ö	yrValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuPro 45	431	Оу
64	CCCCTGCCCTCTGAGACTGATGGCTACGTTGCCCCCCTGACCTTGCAGCCCCCAAGCCTGAA 35	3505	DЪ
õ	oLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlu 43	411	Qy
04	CAAAGCCTCCCCACACATGACCCCCAGCCCTTACAGCGGTACAGTGAGGACCCCACAGTA 35	3445	Db .
10	lnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal 4	391	Qy
144	AAGGGGCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGG	3385	da
ŏ	lyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 39	371	Qy
84	CTGACACTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCC 33	3325	дь
	euThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer 37	351	Qy
324	GCTGGGGGCATGGTCCACCACAGGCACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGGAC 33	3265	. Db
ŏ,	laGlyGlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAsp 35	331	Qy
264	GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGC 32	3205	da
ŏ.	1у зз	330	Оу
204	ACCIGGIG 32	3145	Дb
29	32	329	Оу
3144	ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	3085	Db
29	32	329	Ωу
084	TGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGC 30	3025	Дb
29	32	329	Оу
024	GAGCGGCTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT 30	2965	Db
9	32	329	Qy
964	GGGG 29	2905	Db
. 68	32	329	Qy
904	TGACTTTT 29	2845	Db
29	.; ω	329	Оу
344	GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG 28	2785	Db
29	32	329	Оу
784	CCAT 27	2725	DЪ
9	32	329	Оу
724	CCAACCAT 27	2665	Db
29	32	329	ОУ
564	TCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGAT 26	2605	Db

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RESULT 11
RESULT 11
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               The invention relates to treating a tumour in a mammal, where the tumour is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does.not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, overy, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; brea stomach; endometrium; salivary gland; lung; kldney; colon; colo thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder;
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                                                                                                                                                                                                                                            Treating tumour characterised by factor receptor, ErbB or cancer anti-ErbB antibody-maytansinoid
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 breast cancer or an aggressive for overexpresses ErbB2. The method
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neuronal, glial, astrocytal, hypothalamic, glandular, macrophaga epithelial, stromal, blastcocoelic, inflammatory, anglogenic and immunological disorders. This sequence represents a HER2 (ErbB2) transgene plasmid construct used to direct expression of native HER2 in the mammary gland of a transgenic mouse.
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ğ	1695	1695 CGCCCGCGCCCTCCCAGCCGGGTCCAGCCGGAGCCATGGAGCTGGCGGCC 1745	
Ϋ́	22	22 LeuPhePheTrpLeuAspArgSerValLeuAlaLysGluLeuAlaArgGlylaAlaAlaSer 41	
ğ	1746	1746 TIGTGCCGCTGGGGGCTCCTCCTCGCCCTTTGCCCCCCGGAGCCGCGAGC 1796	•
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TyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArgIleVal 121 TACGTGCTCATCGCTCACAACCAAGTGAGGCCAGGTCCCCACTGCAGAGGCTGCGGATTGTG 141 2036

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ArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeuCys

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GlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHisSerGly GGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGCCGCCATGAGCAGTGTGCTGCC 2516 2456 281

329 329	Qy	
4617 TCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCCAGGGAC 4676	Db '	3537 GGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAGGGCGCA 3596
	γ	329 329
CAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATGATTGAC		3477 CAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCTTCTGCGTGGCCCGCTGCCCCAGC 3536
	Qy	329 329
TACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGGCTGCCC		3417 TGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAGGCTGAC 3476
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AGTGATGTGTAGGTGTGTGTGTGGGAGCTGATGACTTTTGGGGCCCAAACCT		3357 GAATGCCGAGTACTGCAGGGGCTCCCCCAGGGAGTATGTGAATGCCAGGCACTGTTTGCCG 3416
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ANGGTGCCCATCANGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACCCAG		3297 CCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCCAGGAGTGCGTGGAG 3356
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320		3237 GAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCGAGGGCACTGCTGGGGT 3296
		329 329
CACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAAATTACA		3177 GACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCAGAGGAC 3236
329	Oy	329 329
CTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGGCTCGTA		3117 AGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGTGCCCTGG 3176
		329 329
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		329 329
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		2877 GGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTTGAGACT 2936
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GTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATCCCTGAT		329 329
329 329	Qy	2757 TATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCCAGTTACCAGTGCCAATATCCAG 2816
3837 AGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTGAGGAAG 3896		
329 329	Qy	ACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGAGTGTGC
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329 329	Qy	ATCTGTGAGCTGCACTGCCCAGCCCTGGTCACCACACACA
3597 TGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGATGACAAGGGCTGC 3656	שם	11eCysGluLeuH1sCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMet 301
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        the SPLICE erbB-2 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder; wound healing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a SPLICE erbB-2 receptor protein protein has an in-frame deletion of 16 amino acids, 2 of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding an erbB 2 receptor protein erbB-2, inhibitors of the protein are useful for
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ProGluThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGly
                                                                          GGAGCCGCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGT
                                                                                                    GlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSer
                                                                                                                                                                         GAGCTGGCGGCCTTGTGCCGCTGG------GGGCTCCTCCTCGCCCCTCTTGCCCCCC
                                                                                                                                                                                                                        PheLeuPheLeuLeuPhePheTrpLeuAspArgSerValLeuAlaLysGluLeuAlaArg
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2449 ACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC 2508	Db	1369 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 1428
329 329	Qy	
2389 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2448	Db	GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG
329 329	Оу	
2329 GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATC 2388	Db	GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAAGCCTGGCATTTCTGCCG
329 329	Qy	
2269 CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG 2328	рb	GCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGAGTTACCACT
329 329	Qy	
2209 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG 2268	ממ	1129 AACCAAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGT 1188
329 329	Qy	
2149 GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGTCTTTGGGATCCTCATCAAGCGACGG 2208	. · dd	1069 TGTCCCTACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTTCTCCAC 1128
329 329	Qy	
2089 GACAAGGGCTGCCCGGCGGAGCAGAGAGCCAGCCCTCTGACGTCCATCATCTCTGCGGTG 2148	Db	1009 TIPIGAGETCASTELLA CONTROLLE
329 329	Qy	
2029 GAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGAT 2088	Db	**************************************
329 329	. ογ	AanH1aGarG1v1]aGvaG1v10v14fcGvaGr0A1a10vValHhrHvrAppHhrxopHhr
1969 CGCTGCCCCAGCGGTGTGAAACCTGACCTCCTACATGCCCCATCTGGAAGTTTCCAGAT 2028	Db	CAGTGTGCTGCCGGCTGCACGGGCCCCAAGCACTCTGACTGCCTTGGCCTTGCCTTCCACTTC
329 329	Qy	GinCvsAlaAlaGlvCvsThrGlvProLvsHisSerAspCvsLenAla
1909 CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT	Db	
329 329	Оу	Va CvsA aC vC vCvsA aArrCvsC vsC v
1849 CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA 1908	ממ	
329 329	. Оу	CvsLvsGlvSerArgCvsTrpGlvGluSerSerGluAspCvsGlnSerIeuThrArgThr
1789 GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCCAGGGAGTATGTGAATGCCAGG 18∮8	. Db	
329 329	Qy	
1729 CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCCTTCGGGGCCAG 1788	, pb	
329 329	. Оу	Drof nl nl veffvrf naenfhrt of nl rol veffvrf nahout nt veffvrf nanout veffvrf veffvrf
1669 CGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCGAGGG 1728	da	C44.05.034.00.04.00.00.00.00.00.00.00.00.00.00.00
329 329	Qy	GlufeniGlnTenArraserTenyThrGlnTle1eTenyTvsGlvGlvGlvTile1Tle61nArraser
1609 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC 1668	מם	
329 329	Qy	AsnGlvAspDroLeuAsnAsnThrThrDroValThrGlvAlaserDroGlvGlvLeuAra 1
1549 AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 1608	ДЪ	
329 329	. Oy	[.ellArg[]eVa]ArgG vThrG nLellBheG llAspasnTvralaTellaVa]I ellasp
1489 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGGCTGGGGCTGCGCTCACTG 1548	מם	
329 329	Оу	GluValGlnGlvTvrValLeuTlealaH;sasnGlnValaraGlnValBroTonGlnAra
1429 CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGGACGAATTCTGCACAAT 1488	da	1
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430 3588	ASPG1YTYrValAlaProLeuThrCysSerProG1nProG1u 	D 04
410 3528	391 GlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal 	망
390 3468	VValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 	DP QA
370 3408	351 LeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer 	р Q
350 3348	331 AlaGlyGlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAsp 	Db Qy
3288	3229 GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGC	B 4
3228	69 CCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTG	ag.
329	329	Ωу
3168	3109 ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	용
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3108	TCTGAATTCTCCCGC	망
329		Qy
3048	2989 GAGCGGCTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT	Db
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2988	2929 GGGGCCAAACCTTACGATGGGATCCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGG	Db
329	329	Q
2928	2869 TTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTT	Db
329	329	Qy
2868	2809 GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG	뮍
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2808	2749 GTCAAAATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTGACGAGACAGAGTACCAT	망
329	329	9
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2628	2569 CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGC	В
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This is the human HER-2 polynucleotide sequence. The HER-2 gene also called c-neu and ErbB2, encodes a transmembrane receptor, with tyrosine kinase activity. HER-2 is related to the epidermal growth factor receptor (BEFR or HER-1). Aberrant HER-2 expression is present in a wide number of cancers, especially breast, ovarian and gastric cancers. This sequence is used in the invention to design 12-25 nucleotide oligonucleotides that decrease the expression of human HER-2. The oligonucleotides of the invention (AAZ31067-Z31070) can also be used for modulating the expression of human epidermal growth factor receptor. The oligonucleotides are used to treat diseases or conditions associated with
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                                                                                                                                                                 New antisense sequences especially cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                     HER-2; c-neu; BrbB2; transmembrane receptor; tyrosine kinase activity; epidermal growth factor receptor; EGFR; HER-1; cancer; breast cancer; ovarian cancer; gastric cancer; antisense oligonucleotide; expression; hyperproliferative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ31071;
                                                                                                                                        Examples; Page 38-39; 44pp; English
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                                                                                                                                                                                                                              Bennett CF,
                                                                                                                                                                                                                                                      (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HER-2 nucleic acid sequence
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4473 BP; 902 Av. 1383 C; 1329 C; 859 T; 0 other: 1.328 - 902 Av. 1383 C; 1329 C; 859 T; 0 other: 2.328	CGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCGAGGG	. Db		
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articularly hyperproliferative diseases such as cancer. Oy 298 PheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla 11 11 11 11 11 11 11	9	Оу	64.67% Indels: 73	Query Ma
ER-2, particularly hyperproliferative diseases such as cancer. Oy 298 PheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla	8 CysProTyrAsnTyrLeuSerThrAspValGlySer	dq Vo	1.33e-97 Length: 447 2418.00 Matches: 523 arity: 41.66% Conservative: 5.	Pred. No Score: Percent
HER-2, particularly hyperproliferative diseases such as cancer. Oy 298 PheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla	TTTGAGTCCATGCCCAATCCCGAGGCCGGTATACATTCGGCGCCCAGCTGTGTGAGCTGCC	מם	ence 44/3 BF; 902 A; 1383 C; 1329 G; 859 T; 0 Scores:	Alignmen
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В	2809	GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG	2868	
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316 CCCTTGGACAGACTTCTACCGCTCACTGCTGGAGACGACGACTGACATGGGGACCTGGTG 3228 330	FT	SO XX	XX X X X	X E	X D	ኒ አ	Q	RESU	DВ	Qγ	Db	Qγ	ф	Qy	Db	Qγ	Db	Qγ	Db	Qy	Db	Qy	Db	νQ	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Дb	Qy	Db
CCTTGGACCACCTCTACCGCTCACTGGAGGACATGAGACATGGGGACCTGGTG 3228 laGlyGlyMetvalHisHisArgHisArgSerSerSerSerThrargSerGlyGlyGlyAsp 350 cracGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTTCTGTCCAGCACCCTGCCCGGGC 2288 laGlyGlyMetvalHisHisArgHisArgSerSerSerSerThrargSerGlyGlyAsp 350 cracGCCTGGCCCCCCCCCCCCCCCCCCCCCCCCCTCTCACCAGGGGCTGGGGCCTGGGAC 3348 cracGCTGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	D 0	Homo	Huma hype tumo	D)	3-8	Ü	AAD3	7	94	Ġ	88	ū	82	Ė	76	9	70	7	64	S	58	w	52	411	46	9	40	7	34		28	ŵ	22	w	16
228 30 55 50 31 44 40 40 40 40 40 40 40 40 40 40 40 40	cation/Qualifier 53942	apiens.	Her-2; epidermal growth factor receptor 2; infection; cance roliferative disorder; prophylaxis; inflammation; antisense; gene therapy; phosphorothioate backbone; gene; ss.	Her-2 [P-2002 (first entry)	904;	904 standard; DNA; 4473 BP.		CCAGAAGGCCAAGTCCG 3960	laArgSerProSerPro 55		lyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProAlaAlaAlaPro 5	CTCTATTACTGGGACCAGGACCCACCAGCAGCGGGGGGCTCCACCCAGCACCTTCAAA 3	LeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLys		roGlnGlyGlyAlaAlaProGlnProH1sProProProAlaPheSerProAlaPheAsp		${f lyValValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThr}$ 4		gProAlaGlyAlaThrLeuGluArgAlaLysThrLeuSerProGlyLysAsn 4	ATGTGAACCAGCCAGATGTTCGGCCCCAGCCCCCTTCGCCCCGAGAGGGCCCCCTTCGCCT 3	yrValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuPro 4	CCTGCCCTCTGAGACTGATGCTACGTTGCCCCCTGACCTGCAGCCCCCAGCCTGAA 3	roLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlu 4		lnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal 4	AAGGGGCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTG 3	luGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 3	CACTAGGGCTGGAGCCCTCTGAAGAGAGGCCCCCAGGTCTCCACTGGCACCCTCC 3	hrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer 3	CTGGGGGCATGGTCCACCACAGGCACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGAC 3	laGlyGlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAsp 3	ATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGC 3	Gly 3	CTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTG 3
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                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4473
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LeuArgIleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAsp
                              GAGCTGGCGGCCTTGTGCCGCTGG------GGGCTCCTCCTCGCCCTCTTGCCCCCC
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                                                                                                                         The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. particular, the antibody is directed against ErbB2 (also known as HE and pl85neu). The method is particularly useful in the treatment of breast, overian, stomach, endometrial, salivary gland, lung, kidney, breast, overian, stomach, endometrial, salivary gland, lung, kidney,
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	3776	17 CTGGTCGTCGTCTTGGGGGTCGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATC	b 3717
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	3536	7 CAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCTTCTGCGTGGCCCGCTGCCCCAGC)b 3477
	329	9)у 329
	3476	7 TGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAGGCTGAC	b 3417
_	329	29)у 329
	3416	7 GAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGTTTGCCG)b 3357
	329	9	у 329
	3356)7 CCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGGCCAGGAGTGCGTGGAG)b 3297
	329	19)y 329
	3296	7 GAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCCGAGGGCACTGCTGGGGT	b 3237
	329	9	у 329
	3236	7 GACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCAGAGGAC)b 3177
	329	99)у 329
	3176	.7 AGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCACACGGTGCCCTGG	b 3117
	329 .	19)у 329
	3116	7 CTGACCCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGAACTGGGC)b 3057
	329	99)у 329
	3056	7 AGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGCCTACTCG	b 2997
	329)у 329
	2996	7 CTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCCTGCCT	b 2937
	329	.9)у 329
	2936	7 GGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTTGAGACT	ъ 2877
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	2876	7 GAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGCTTTGAT	b 2817
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Search completed: May 8, 2003, 13:04:15 Job time: 1665 secs

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-WODEL-frame+_p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/US9821883/runat_28042003_104749_14566/app_query.fasta_1.839
-Q-/cgn2_1/USPTO_spool/US9821883/runat_28042003_104749_14566/app_query.fasta_1.839
-DB-GenEmbl -OFMT-fastap -SUFFIX-p2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEARSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US9821883_GCGN_1 _3745_Grunat_28042003_104749_14566 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THEADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

Qy 201 ThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGly 220		Qy 161 LeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGlnLeu 180	ProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeuGln 			Qy 81 LeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGln 100	61 HisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeuGlu 80 	Oy .41 SerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThr 60		Qy 1 MetArgAlaAlaProLeuLeuLeuAlaArgAlaAlaSerLeuSerLeuGlyPheLeuPhe 20	y Match: 100.00% Indels: 6 Gaps: 9-821-883-2 (1-690) x Ax268286 (1-2070)	5.18e-129 Length: 3739.00 Matches: 100.00% Conservati	425 a	source 12070 source 12070 source /organism="synthetic construct" /db_xref="taxon:2630"	TITLE Compositions and methods for dendritic cell-based immunotherapy JOURNAL Patent: WO 0174855-A 7 11-OCT-2001; DENDREON CORPORATION (US) FEATURES LOCALIAN CONSISTENCY.	X	AX268286 AX268286.1 GI:16541538 Synthetic construct.	AX268286 AX268286 2070 bp DNA linear PAT 29-OCT-2001 DEFINITION Sequence 7 from Patent W00174855.	
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	Pred. No.: 2.69e-119 Length: 2091 Score: Score: 9473.50 Matches: 641 Percent Similarity: 94.42% Conservative: 19 Best Local Similarity: 91.70% Mismatches: 28 Query Match: 92.90% Indels: 11 DB: 6 Gaps: 2 US-09-821-883-2 (1-690) x AX268288 (1-2091)	ં છે	M synthetic artificial artificial compositio compositio patent: WC patent: WC pendreon c	RESULT 2 AX268288 AX268288 LOCUS AX268288 DEFINITION Sequence 9 from Patent WO0174855. ACCESSION AX268288 VERSION AX268288.1 GI:16541540 KEYWORDS SOURCE synthetic construct	QY 61 PRELEUREVALILEPTOPHEASCYSTIPG LIBERTOVALGING LIGITALIZATEPTOPTO 680	1861 CTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACAACAGCACTGCCCTCCAACCCCG 641 GluThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAsp	Oy 601 ThrCysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLys 620	Db 1681 TGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGGAGACACT 1740 Qy 581 AlaalaGlumetAsnGluThrValGluValIleSerGlumetPheAspLeuGlnGluPro 600
	Qy Qy Db	Oy Ob	Оу Оу	Оу Оу Ор	оу Оу ор	Db Qy Db	Qу ДЪ	Db Qу Db
352 ThrLeuGlyLeuGluproSerGluGluGluAlaProArgSerProLeuAlaProSerGlu 371	321 ASNTYPLEUSETTHRASPVALGLYSET	281 GlyIleCysGluLeuHiSCysProAlaLeuValThrTyrAsnThrAspThrPheGluSer 300	241 GlyClyCysAlaArgCysLysGlyProLeuProThrAspCysCysH1sGluGlnCysAla 260	201 ThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGly 220	161 LeulargSerLeuThrGluIleLeulaySGLyGlyValLeuIleGlnArgAsnProGlaLeu 180		101 GlyTyrValLeuIleAlaH1sAsnGlnValArgGlnValProLeuGlnArgLeuArgIle 120	181 CACCTGGACATGCTCCGCCACCTCTACCAGGGCTGCCAGGTGGTGCAGGGAAACCTGGAA 240 81 LeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGln 100 81

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                    Laus,R., Vidovic,D. and Graddis,T.
Compositions and methods for dendritic
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Qy 201 ThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGly 220	Qy 121 ValargGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAsp 140	Db 61 CTGCTTTTTTTCTGGCTAGACCGAAGTGTACTAGCCAAGAGTTGGCGCGCGGGGCCCCC 120 Qy 41 SerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThr 60 [ORIGIN Alignment Scores: Pred. No.: 2959.50 Score: Percent Similarity: 97.88% Best Local Similarity: 79.15% Query Match: US-09-821-883-2 (1-690) x Ax268287 (1-1692) Oy 1 MetArgAlaAlaProLeuLeuAlaArgAlaAlaSerLeuSerLeuGlyPheLeuPhe Db 1 ATGAGAGCTGCACCCCTCCTGGCCAGGCCAGAGCCTTAGCCTTGGTTT 60 Oy 21 LeuLeuPhePhePrpLeuAspArgSerValLeuAlaArgGluCaAgGCCTTAGCCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG

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Halpern,M.S. and England,J.M.
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                                                                                       ValCysAlaG1yG1yCysAlaArgCysLysG1yProLeuProThrAspCysCysH1sG1u
                                                                                                                      CysLysGlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLepThrArgThr
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PheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla
                       AsnHisSerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThr
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2905 GGGGCCAAACCTTACGATGGGATCCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGG 2964	Db	CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA
329 329	Qy	
2845 TTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTT 2904	Db	GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGG
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329 329	ОУ	
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CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGC	Db	1465 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTG
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2485 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA 2544	Db	1405 CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGGACGAATTCTGCACAAT 1464
329 329	Qy	
2425 ACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC 2484	Db	1345 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 1404
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2365 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2424	Db	GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG
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2305 GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATC 2364	dd	GCGAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAAGCTTTTGGGAAGCTTTTTGTGCG
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2245 CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAJAGACG 2304	Db	GCCCGAGTGTGCTATGGTCTGGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGT
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2125 GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGG 2184	ДĎ	
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                                  Nicolette, C.A.
Therapeutic compounds
Patent: WO 0168677-A 1 20-SEP-2001;
GENZYME CORPORATION (US)
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AX282577
                                                                                             Eukaryota;
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/organism="Homo sapiens"
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Alignment Scores: 1.49e-80 Length: 4530 Fored. No.: 2423.00 Matches: 524 Forecent Similarity: 41.14% Conservative: 5 Forest Local Similarity: 40.75% Mismatches: 21 Forest Match: 64.80% Indels: 736 Forest Match: 65.80% Gaps: 4 Forest Match: 1089: 40.75% Gaps: 4 Forest Match: 1089: 40.75% Gaps: 4 Forest Match: 1089: 4 Forest Match

	329	85 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC 1	29	1525 AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 1584	329 329	1465 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTG	329 329	1405 CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAAT 1464	329 329	1345 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 1404	: ω	1285 GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG	329 329	25. GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG	32	1165 GCCCGAGTGTGCTATGGTCTGGGCATGGAGGACTTGCGAGAGGTGAGGGCAGTTACCAGT 1224	329 329	AACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCCTGT 1	329 329		w	85 TTTGAGTCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGACTGCC	98 PheGlusorMetProAsnProGluglvArgTvrThrPheGlvAlasorCvsValThrAla 31	25 AACCACAGTGGCATCTGTGAGCTGCACGTGCCCAGGCCCTAGGTCACACACA	78 AsnHisserGlvTleCvsGluIeuHisCvsDroAlaLeuValThrTvrAsnThrAsnThrAsnThr	0.77 0.78	GIRCIGIA I BALBOTI GENERADA CINCULOR CINCULAR CINCULAR CINCULOR CI	\data	TO TO THE PROPERTY OF THE PROP	218	CINNCICICACACIGATANACACCAAACCACTCTCTCGAACCCCTGTTCTCCGAAC	98 LeuAlaLeuThrLeuILeAspThrAsnArgSerArgAlaCysHlsProCysSerProMet 21	S CCCCAGCTCTGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAG	78 ProGlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheH:sLysAsnAsnGln 19	S GASCTSCAGCTTCSAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCCAGCGGAAC 6		
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QΥ	329	32	9
ф	2905	CTGCTGGAAAAGGGG 29	64
Qy	329	32	
Вb	2965	GAGCGGCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT 30	24
γo	329	32	9
₽	3025	TCTCCCGC 30	84
Qy	329	32	9
문	3085	ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	44
Ŷ	329	32	9
뭥	3145	CCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTG 32	04
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Вb	3205	GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGC 32	64
δÃ	w	AlaGlyGlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAsp 35	0
В	3265	CTGGGGGCATGGTCCACCACAGGCACCGCAGCTCATCTACCAGGAGTGGGGGTGGGGAC 33	24
B 8	351 3325	LeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer 37	84
Qy	371	luGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 39	0
d 0	3385	GAAGGGCTGCCATGTATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTG 34	44
Qy	391	GlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal 41	0
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용	3805	ACTGGGACCAGGACCÇACCAGAGCGGGGGGCTCCACCCAGCACCTTCAAA 38	64

Qy 7 Db 32 Qy 9	Qy 5 Db 26	Оу 3 рь 20	Qy 1 Db 15	Qy Db 9	US-09-82	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	Sourc BASE COUNT ORIGIN	FEATURES		COMMENT	REFERENCE AUTHORS TITLE JOURNAL	VERSION KEYWORDS SOURCE ORGANISM	RESULT 7 BD005474 LOCUS DEFINITION ACCESSION	Qy 551 Db 3919	Oy 531
78 AsnLeuGluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspfleGln	58 ProGluThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGly 	38 GlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSer 	18 PheLeuPheLeuLeuPhePheTrpLeuAspArgSerValLeuAlaLysGluLeuAlaArg	2 ArgAlaAlaProLeuLeuAlaArgAlaAlaSerLeuSerLeuGly	121-883-2 (1-690) x BD005474 (1-4530)	ores:	rce 14530 /organism /db_xref: NT 922 a 1382	CC TO FH Ke FT SO	PF 13-JAN-1997 JP 1997526124 PR 19-JAN-1996 US 60/010262 PI MICHAEL S HALPERN, JAMES M ENGLAND PC A01K63/00,A61K39/00,A61K39/38,A61K48/00,C12N5/00,	upoutn octonor		BD005 JP 20 unide	7 4 BD005474 4530 bp DNA linear PAT 31- ION Cellular immunogens useful cancer vaccines.	551 AlaargSerProSerPro 556 	31 GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProAlaAlaAlaPro
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8	2785	CCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG 2	844
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8	2905	GGGGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGG 29	964
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8	2965	GAGCGGCTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT 30	024
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8	3025	TGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGC 30	084
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8	3085	ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	144
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Ą	331 ·	AlaGlyGlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyAsp 35	50
8	3265	CTGGGGGCATGGTCCACCACAGGCACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGAC 3	324
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¥	451	AlaAlaArgProAlaGlyAlaThrLeuGluArgAlaLysThrLeuSerProGlyLysAsn 47	70
8	3625	TGCCCGACCTGCTGGTGCCACTCTGGAAAGGGCCAAGACTCTCTCCCCAGGGAAGAAT 3	684

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QУ	Фу .	Ф	Оy	Фр	Ф	US-09	Align Pred. Score Perce Best Duery DB:	Db 368 Qy 49 Db 374 Qy 51 Db 380 Qy 53 Db 386 Qy 55 Db 386 Qy 55 Db 386 Qy 55 Db 386 Qy 55 Db 386 Qy 57 DC 386 QY 57 DC 386 DC 391 RESULT 8 LOLL 124 LOLL	Qγ
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320	2545 CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGC 2604		2485 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA 2544	329 329	2425 ACATCCCCCAAAGCCAACAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC 2484	329 329	2365 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2424		GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATC	2245 COGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATGCCTGAAAGAGACG 2304		2185 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG 2244	329 329	2125 GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTCGTCTTTGGGATCCTCATCAAGCGACGG 2184	329 329	2065 GACAAGGGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTG 2124	329 329	2005 GAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGAT 2064	329 329	1945 CGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGAT 2004		329	CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA	329 329 .	1765 GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCCAGGGAGTATGTGAATGCCAGG 1824	329 329	CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG		329 329	CGGCCAGAGGACGAGTGTGTGGGGCGAGGGCCTGGCCTG	CGGCCAGAGGACGAGTGTGTGGGGCGAGGGCCTGGCCTG	ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC

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:lyValValLysAspValPheAlaPhe 	llaAlaArgProAlaGlyAlaThrLeu 	YrValAsnGlnProAspValArgPro 	roLeuProSerGluThrAspGlyTyr CCTGCCCTCTGAGACTGATGGCTAC	lnSerLeuProThrHisAspProSer 	31uG1yA1aG1ySerAspVa1PheAsp 	.euThrLeuGlyLeuGluProSerGlu 	\laGlyGlyMetValHisHisArgHis 	ATGCTGAGGAGTATCTGGTACCCCAG	CCCTTGGACAGCACCTTCTACCGCTCA		\TGGCCAGGGACCCCCAGCGCTTTGTG		TGGATGATTGACTCTGAATGTCGGCCA	;AGCGGCTGCCCCAGCCCCCCATCTGC		GGGGCCAAACCTTACGATGGGATCCCA		TTCACCCACCAGAGTGATGTGTGGAGT		GCAGATGGGGGGAAGGTGCCCATCAAG	GTCAAAATTACAGACTTCGGGCTGGCT)TGCGGCTCGTACACAGGGACTTGGCC		ひんせん よじん カンションマイ ジェンジェンフ マンフィンシャ
lyValValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThr	AlaAlaArgProAlaGlyAlaThrLeuGluArgAlaLySThrLeuSerProGlyLySASn 	TyrValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuPro	ProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlu 	GlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal 	GluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 	LeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer 	AlaGlyGlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAsp 	GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGC	CTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTG		ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG		GATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGGTTGGTGTGTGT	GAGCGGCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT		GGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGG		АСССАССАGAGTGATGTGTGTGAGTTATGGTGTGTGTGTGTGGGGAGGTGATGA		######################################	AAAATTACAGACTTCGGGCTGGCTCGGCTGGACATTGACGAGACAGAGTACCAT		GTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAT	CAPATI DECEMBER OF THE CITE OF THE CONTROL OF THE C	ずくしょく ごしょうしゅ しょうじゅうしゅく ししじんしゅく フェルタ ことしに ないしん マン・シー・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・
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117	98 GluValGlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArg 1 	Qy 3	
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17. 153	2 ArgAlaAlaProLeuLeuLeuAlaArgAlaAlaSerLeuSerLeuGly 1	Qy Db	
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	t Scores: 1.49e-80 Length: 4530	Alignment Pred. No. Score: Percent S Best Loca. Query Matt	
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	1 (bases 1 to 4530) Raziuddin and Sarkar, F. Hoque. Antibody to ERBB2 promoter binding factor Patent: US 5654406-A 9 05-AUG-1997; Location/Qualifiers 1. 4530	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUR	
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	V Sequence 9 from patent US 5654406. 159745 159745.1 GI:2478377	DEFINITION ACCESSION VERSION KEYWORDS	
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	51 AlaArgSerProSerPro 556	Qy 5 Db 39	
550 3918	31 GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProAlaAlaAlaPro 5	Оу 5 Db 38	
530 3864	11 AsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLys 5	Qy 5 Db 38	
510 3804	91 ProGlnGlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAsp 5	Qy 4 Db 37	
3744	85 GGGGTCGTCAAAGACGTTTTTGCCTTTGGGGGGTGCCGTGGAGAACCCCCGAGTACTTGACA 3	Db 36	

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2605 TCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGAT 2664	дь		
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2545 CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGGAAAACCGCGGGACGCCTGGGC 2604	Db		1465 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTG
329 329	Qy		329
2485 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA 2544	Db		1405 CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAAT
329 329	Qy		
2425 ACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC 2484	Db		1345 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC
329 329	Qy		
2365 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC 2424	ДD		1985 GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGGGAGCAGCTTCCAA
329 329	Qy		
2305 GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATC 2364	Db		1925 GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG
329 329	Оу		
2245 CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG 2304	ф		1 6.5 (2000) 6.5 (2000) 7.5 (2000)
329 329	Qy		
2185 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG 2244	Дb		1105 - БАКССБАКСИТСЯКСАСАСКАСКАТССВАСАССВЕТСИКАСБАКСИСТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОСТВОТОВОТО
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329 329	Qy		
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329 329			
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1825 CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCCAGAATGGCTCAGTGACCTGTTTTGGA 1884	Db		**************************************
329 329	Оу		
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329 329	ОУ		
1705 CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG 1764	Db		24 COMENCE AND THE PROPERTY OF A CONTROL OF
329 329	Оу		
1645 CGGCCAGAGGACGAGTGTGTGGGGCGAGGGCCTGGCCTG	Db		TO GALLEGUAL MARKET TO SALLEGUAL TO SALLEGUA
329 329	Qy		
1585 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC 1644	Db		
329 329	Qy		
1525 AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC 1584	Дb		

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ş	329		329
В	2665	GTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAT	2724
VΩ	329		329
В	2725	GTCAAAATTACAGACTTCGGGCTGGCTCGGCTGGACATTGACGAGACAGAGTACCAT	2784
γo	329		329
₽	2785	GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG	2844
VΩ	329		329
В	2845	TTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTT :	2904
γo	329		329 .
망	2905	GGGGCCAAACCTTACGATGGGATCCCCAGCCCGGGAGATCCCCTGACCTGCTGGAAAAGGGG	2964
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망	2965	ATTGATGTCTACATGATCATGGTCAAATGT	3024
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Ф	3025	GTGTCTGAATTCTCCCGC	3084
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βb	3085	ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	3144
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γ	330	G1y	330
В	3205	GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCCTGCCCCGGGC	3264
δ	331	AlaGlyGlyMetValHisHisArgHisArgSerSerSerSerThrArgSerGlyGlyGlyAsp	350
Dβ	3265	CTGGGGGCATGGTCCACCACAGGCACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGAC	3324
ν	351	LeuThrLeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSer	370
В	3325	CACTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCC	3384
γQ	7	GluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLySGlýLeu	390
Б	3385	AAGGGCTGCCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCCTG	3444
γ	391	GlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal	410
В	3445	AAAGCCTCCCCACACATGACCCCAGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTA	3504
γQ	411	ProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlu	430
₽	3505	CCCTGCCCTCTGAGACTGATGGCTACGTTGCCCCCTGACCTGCAGCCCCAGCCTGAA	3564
Q	431	TyrValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuPro	450
Ф	3565	ATGTGAACCAGCCAGATGTTCGGCCCCAGCCCCTTCGCCCCGAGAGGGCCCCTCTGCCT	3624
Ş	451	- =	470
₽	3625	CTGCCCGACCTGCTGCTACTCTGGAAAGGGCCAAGACTCTCTCCCCAGGGAAGAAT	3684
δ	7	GlyValValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThr	490
망	3685	GGGTCGTCAAAGACGTTTTTGCCTTTGGGGGGTGCCGTGGAGAACCCCGAGTACTTGACA	3744

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coussens, L., Yang-Feng, T.L., Liao, Y.-C., Chen, E., Gray, A., McGrath, J., Seeburg, P.H., Libermann, T.A., Schlessinger, J., Francke, U., Levinson, A. and Ulirich, A.

Tyrosine kinasa roccara.
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Homo sapiens
Eukaryota; Metazoa; Chordata: Craniata. Vortoberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1988)
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Ullrich, A.
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tyrosine kinase-type receptor (HER2) mRNA, o
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Qy 278 AsnHisSerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThr 297	Oy 258 GlnCysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPhe 277	Qy 238 ValCysAlaGlyClyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlu 257	218 745	OY 198 LOUALALOUTRILOUILEASPTRIASRATGSETATGALACYSHISPTOCYSSETPTOMET 217	625 CCCCAGCTCTGCCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAG 684	177 624	Qy 138 AsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArg 157	Oy 118 LeuArgIleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAsp 137	Qy 98 GluValGlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArg 117	Oy 78 AsnieuGluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspileGln 97	Qy 58 ProGluThrHisLeuAspMetLeuArgHIsLeuTyrGlnGlyCysGlnValValGlnGly 77	Qy 38 GlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSer 57	Qy 18 PheLeuPheLeuLeuPhePheTrpLeuAspArgSerValLeuAlaLysGluLeuAlaArg 37	QY 2 ArgAlaAlaProLeuLeuAlaArgAlaAlaSerLeuSerLeuGly 17	x HUMHER2A (1-4530)	Pred. No.: 1.49e-80 Length: 4530 Score: 2423.00 Matches: 524 Percent Similarity: 41.14% Conservative: 5 Best Local Similarity: 40.75% Mismatches: 21 Query Match: 64.80% Indels: 736 DB: 9 Gaps: 4	POPHPPARSPAFDALYYMDODPPERGAPPSTFKGTPTAENPEXLGLDVPV" old_sequence 1701. 1719 /citation=[1] BASE COUNT 922 a 1382 c 1346 g 880 t ORIGIN Chromosome 17q21-q22.
_	. Db	ob Ov	ob Qy	Ç.‡ Db	Ор	. Ob	Qy Qy	Ov S	Db .	Ov Cv	Db J	Ov b	ob C	ob Oy	Db	, od Oy	од Оу
263	1945 CGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCCAGAT	1885 CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT	1825 CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACOTGTTTTGGA	1765 GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCCAGGGAGTATGTGAATGCCAGG 1824	1705 CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG 1764	1645 CGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCGAGGG	1585 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC	1525 AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC	1465 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTTGGGGCTGCGCTCACTG	140	1345 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC	1285 GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCCCCC	1225 GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG	329 1165 GCCCGAGTGTGCTATGGTCTGGGGCATGGAGCACTTGCGAGAGGGTGAGGGCAGTTACCAGT 1224 329	1105 AACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGT	318 CysProTyrAsnTyrLeuSerThrAspValGlySer 329	925 AACCACAGTGGCATCTGTGAGCTGCACTGCCCAGCCCTGGTCACCTACAACACAGACACAGACACG 984 298 PheGluSerMetProAgnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla 317

3144	3085 ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	В
329	329	Qy
3084	3025 TGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGC	DЬ
329	329	Qy
3024	2965 GAGCGGCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGT	DЬ
329	329	οy
2964	2905 GGGGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGGTGGAAAAGGGG	Ф
329	329	Q
2904	2845 TTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGGAGCTGATGACTTTT	DЪ
329	329	Qy
2844	2785 GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG	рь
329	329	γo
2784	2725 GTCAAAATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTGACGAGAGAGA	DЪ
329	329	Qy
2724	2665 GTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAT	В
329	329	Qy
2664	2605 TCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGAT	DЬ
329	329	Qy
2604	2545 CAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGC	Db
329	329	οy
2544	2485 TCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACA	В
329	329	Qy
2484	2425 ACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGC	В
329	329	γo
2424	2365 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC	рb
329	329	Qy
2364	2305 GAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATC	ф
329	329	γo
2304	2245 CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG	Db
329	329	γQ
2244	2185 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG	Db
329	329	δ
2184	TTGGGATCCTCATCAAGCGACGG	Db
329	329	Qy
2124	2065 GACAAGGGCTGCCCCGCCGAGCAGAGAGCCCAGCCCTCTGACGTCCATCGTCTCTGCGGTG	Ъ
329	329	Qy
2064	2005 GAGGAGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGAT	망

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LOCUS	Qy Db 3 RESULT	Qy Db	Qу	Db Oy	ду	Qу	Db Qy	Db Qy	Qу	Qу	do Vo	Qу	Вb	Qy	B	Qy
OCUS OCUS EFINITION CCESSION ERSION EYWORDS OURCE ORGANISM ORGANISM AUTHORS TITLE JOURNAL	551 3919 T 11	531 3865	511 3805	491 3745	471 3685	451 3625	431 3565	411 3505	391 3445	371 3385	351 3325	331 3265	3205	330	3145	329
AX060703 Sequence 1 from Patent W00100244. AX060703 AX060703.1 GI:12406100 Synthetic construct. Synthetic construct artificial sequences 1 (bases 1 to 9274) Erickson, S. and Schwall, R. Methods of treatment using anti-erbb antibody-maytansinoid conjugates Patent: WO 0100244-A.1 04-JAN-2001; Genentech, Inc. (US)	AlaArgSerProSerPro 556 ACCAGAAGGCCAAGTCCG 3936	GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProAlaAlaAlaPro 550 	AsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLys 530	ProGlnGlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAsp 510	GIYVAlVASLYSASPVAlPheAlaPheGIYGIYAlaValGluAsnProGluTyrLeuThr 490	AlaAlaArgProAlaGlyAlaThrLeuGluArgAlaLysThrLeuSerProGlyLysAsn 470	TyrValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuPro 450	ProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlu 430	GlnSerLeuProThrHisaspProSerProLeuGlnArgTyrSerGluAspProThrVal 410. 	GluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 390 	LeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer 370	AlaGlyGlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAsp 350 	GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGC 3264		CCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTG 3204	329

Oy 182 TyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeuThr 201	121 203 141 209 161 215 181	1695 CGCCCCGCGCCCTCCCAGCCGGGTCCAGCCGAGCCATGGAGCTGGAGCTGGAGCTGCAGCCGCGCGCCCTCCCAGCCGGGTCCAGCCGAGCCATGGAGCTGGAGCTGGCGGCC 1 22 LeuPhePheTrpLeuAspArgSerValLeuAlaLysGluLeuAlaArgGlyAlaAlaSer 4	FEATURES 1.9274 /organism="synthetic construct" /db_xref="taxon:3x530" /note="vector sequence" BASE COUNT 2152 a 2538 c 2489 g 2095 t ORIGIN Alignment Scores: Pred. No.: 2422.00 Pered. No.: 2422.00 Percent Similarity: 41.12% Conservative: 9 Best Local Similarity: 40.43% Mismatches: 31 Query Match: 64.78% Gaps: 6 DB: US-09-821-883-2 (1-690) x AX060703 (1-9274) Ov 2 ArgalaalaProfeurenteral aargalaalaScortengClypholen 21
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97 CCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGCGTGAG 29	329	2757 TATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGTGCCAATATCCAG 2816 329	282 IleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerWet 301

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	329	9	Оу 329
	4676	7 TCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCCAGGGAC	Db 4617
	329	9	Оу 329
	4616	7 CAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATGATTGAC	Db 4557
	329	9	Оу 329
:	4556	7 TACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGGGG	Db 4497
	329	9	Оу 329
	4496	7 AGTGATGTGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGGCCAAACCT	Db 4437
	329	9	Оу 329
	4436	7 AAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACCCACC	Db 4377
	329	9	Оу 329
	4376	7 GACTTCGGGCTGGCTGGCTGGACATTGACGAGACAGAGTACCATGCAGATGGGGGC	рь 4317
	329	9	Оу 329
	4316	7 CACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCCAACCATGTCAAAATTACA	Db 4257
	329	9	Оу 329
	4256	7 CTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGGCTCGTA	Db 4197
	329	9	Оу 329
	4196	7 TATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAGGACCTG	Db 4137
	329	9	Оу 329
	4136	7 TCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTTATGCCC	Db 4077
	329	9	Оу 329
	4076	7 GCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCCATATGTC	Db 4017
	329	9	Оу 329
	4016	7 GGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCCCCCAAA	Db 3957
	329	9	Оу 329
	3956	7 GTGAAGGTGCTTGGATÇTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATCCCTGAT	Db 3897
	329	9	Оу 329
-	3896	7 AGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGAGACGGAGCTGAGGAAG	Db 3837
	329	9	Оу 329
-	3836	7 CGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTGACACCT	Db 3777
	329	ġ	Оу 329
:	3776	7 CTGGTCGTGGTCTTGGGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATC	Db 3717
	329	9	Оу 329
	3716	7 CCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGCATTCTG	Db 3657
	329	9	Оу 329
	3656	7 TGCCAGCCTTGCCCCATCAACTGCACCCACTCCTGTGTGGACCTGGATGACAAGGGCTGC	Db 3597
	329	9	Оу 329

RESULT 12 AR080259 LOCUS DEFINITION Sequence ACCESSION AR080259 VERSION AR080259 KEYWORDS Unknown.	Qy 575 AsnLeuSerAr ::: Db 5562 AGCTATTCCAG	Qy 555 SerProSerTh	Qy 535 AlaGluAsnP Db 5457 GCAGAGAACC	Qy 515 TrpAspGlnAs	Qy 495 AlaAlaProG	Qy 475 AspValPheA	Qy 455 AlaGlyAlaTh	Qy 435 ProAspValA Db 5157 CCAGATGTTC	Qy 415 GluThrAspGlyT 	Qy 395 ThrHisAspPro	Qy 375 SerAspValPh	Qy 355 LeuGluProSe Db 4917 CTGGAGCCCTC	Qy 335 ValHisHisAr 	Qy 330	Db 4737 ACCTTCTACC	Qу 329	Db 4677 CCCCAGCGCT
4473 bp DNA 1 from patent US 5968748. 1 GI:10006994	gAspThr 580 ::: ;AAGTAGT 5579	hrGlnProTrpGluHisValAsnAlaIleGl ::: AAGCCCTGATGTGTCCTCAGGGA	roGluTyrLeuGlyLeuAspValProAlaAl CAGAGTACCTGGGTCTGGACGTGCCA	pProProGluArgGlýAlaProProSerThrP ccaccagagcgggggcTccaccagcaccT	llnProHisProProProAlaPheSerProAl 	llaPheG1yG1yAlaVa1G1uAsnProG1uTy 	rLeuGluargAlaLysThrLeuSerProG] 	ArgProGlnProProSerProArgGluGlyPr 	yrValAlaProLeuThrCysSerProG 	SerProLeuglnArgTyrSerGluAspP: AGCCCTCTACAGCGGTACAGTGAGGACCC	heAspGlyAspLeuGlyMetGlyAlaAlaLys 	rGluGluGlúAlaProArgSerProLeuAl 	gHisargSerSerSerThrargS 	CCCAGCAGGGCTTCTTCTGTCCAGACCCTGC	GCTCACTGCTGGAGGACGATGACATGGGGGA		CTTTGTGGTCATCCAGAATGAGGACTTGGGCCC
linear PAT 31		.nGluAlaArgArgLeuLeu :::: GCAGGGAAGGCGGCCTCTG	AAlaProAlaArgSerPro -GTGTGAACCAGAAGGCCA	rPheLysGlyThrProThr	laPheAspAsnLeuTyrTyr 	PyrLeuThrProGlnGlyGly	yLysasnGlyValValLys 	:oLeuProAlaAlaArgPro 	InProGluTyrValAsnGln 	CACAGTACCCCTGCCCTCT	/SGlyLeuGlnSerLeuPro 	.aProSerGluGlyAlaGly 	erGlyGlyGlyAspLeuThrLeuGly 	GlyAlaGlyGlyMet CCCGGGCGCTGGGGGCATG	ACCTGGTGGATGCTGAGGAG		PAGCCAGTCCCTTGGACAGC
-AUG-2000		574 5561	554 5510	534 5456	514 5396	494 5336	474 5276	454 5216	434 5156	414 5096	394 5036	374 4976 .	354 4916	334 4856	4796	329	4736

HEOREE BERNEE 1 (Dases 1 to 4473) HONS Bennett C. Frank. Lipton, A. and Witters, L.W. PRINCE PATCH C. Frank. Lipton, A. and Witters, L.W. PRINCE PATCH C. Frank. Lipton, A. and Witters, L.W. PRINCE PATCH C. Frank. Lipton, A. and Witters, L.W. Antisense oligonuclecides concluded the model of human HER-2 expression and the patch concluded the	Qy		HisPhe 27	lyProLysH1sSerAspCysLeuAlaCys	Glnc	N (
1 to 4473) 1568748 A. 11 jo.oqr-1999; 2.256-80 1833 c 1329 g 859 t 2.183 c 1329 g 859 t 2.256-80 183 c 1329 g 859 t 2.256-80 184 ches: 523 4.1684 4.1684 184 ches: 72 4.1684 185 c 1329 g 859 t 2.256-80 1.776 c 1329 g 859 t 2.776 c 1329 g 859 t 2.777 c 1329 g 859 t	D 5		HisGlu 2	rgCysLysGlyProLeuProThrAspCys 	Valo	Oy 238	
1 to 4473) 1588748 A. 11 jo.ogr-1999; 20ation/cualifiers 1473 2.256-80	0 ν		œ	SAGAGAGTTCTGAGGATTGTCAGAGCCTG	10	Db 769	
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Trenk. Libron, A. and Witters L.M. 118000Lectide modulation of human HER-2 expression 5588788 A. 13 yo CGT-1999; 2.25e-80 Length: 4473 2.18.00 Matches: 523 44.10% Mismatches: 524 40.57% Mismatches: 736 64.57% Mismatches: 736 64.67% Mismatches: 22 736 737 1111111111111111111111111111111	Db 1	· .		hrAsnArgSerArgAlaCysH1sProCys 	3=2	ОУ 198 Db 709	
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1 to 4473) Frank. Lipton,A. and Witters,L.M. Fignalk. Lipton,A. and Witters,L.M. 5968748-A. 1 19-OCT-1999; coation/Qualifiers .4473 2418.00 Length: 4473 2418.00 Matches: 523 41.06% Conservative: 5 40.67% Indels: 736 46.67% Indels: 736 6 Gaps: 4 2 x AR080259 (1-4473) LeuLeuLeuLalaArgAla	o b			CGCTCACAACCAAGTGAGGCAGGTCCCA		оу 98 рь 409	
1 to 4473) Frank, Lipton, A. and Witters, L.M. 5968748-A 1 19-OCT-1999; cation/Qualifiers .4473 2.25e-80	Qy	•		CCACCAATGCCAGCCTGTCCTTCCTGCAG			
1 to 4473) Frank, Lipton, A. and Witters, L.M. Fignal, Lipton, A. and Witters, L.M. 5968748-A 1 19-OCT-1999; cation/Qualifiers .4473 .7473	B &			roThrAsnAlaSerLeuSerPheLeuGln		Оу 78	
1 to 4473) Frank, Lipton, A. and Witters, L.M. Frank, Lipton, A. and Witters, L.M. 1968748-A 1 19-OCT-1999; coation/Qualifiers 1473 coation/Qualifiers 1473 2.25e-80 Length: 4473 2418.00 Matches: 523 41.06% Conservative: 5 40.67% Mismatches: 22 64.67% Mismatches: 736 6 Gaps: 4 10 x ARO80259 (1-4473) LeuLeuLeuAlargAla	S B 2	· ·	77 34	<pre>puArgHisLeuTyrGlnGlyCysGlnVal </pre>	_	Qy 58 Db 289	
1 to 4473) Frank, Lipton, A. and Witters, L.M. Frank, Lipton, A. and Witters, L.M. Spanismucleoride modulation of human HER-2 expression Spanism-"unknown" 19-0CT-1999; cation/Qualifiers .4473 .4473 .183 c 1329 g 859 t 2.25e-80	d d		28	ysThrGlyThrAspMetLysLeuArgLeu 		Qy 38 Db 229	
1 to 4473) Frank, Lipton, A. and Witters, L.M. Fignal, Lipton, A. and Witters, L.M. Spanicial modulation of human HER-2 expression Spanism-"unknown" Spanism	o d r		37 22	rpLeuAspArgSerValLeuAlaLysGlu 		Oy 18	
1 to 4473) Frank., Lipton, A. and Witters, L.M. Fignal, Lipton, A. and Witters, L.M. Lipton, A. and Witters, L.M. Frank., Lipton, A. and Witters, L.M. Frank., Lipton, A. and Witters, L.M. Frank., Lipton, A. and Witters, L.M. Lipton, A. and Witters, L.M. Length: 2.25e-80	0 B 1			laArgAlaAlaSerLeu :: ::: CCGGAGCCATGGGGCCGGAGCCGCAGTG	-	j	
1 to 4473) Frank, Lipton, A. and Witters, L.M. Frank, Lipton, A. and Witters, L.M. Spantian Control of human HER-2 expression Sp88748-A 1 19-OCT-1999; Cation/Qualifiers -4473 Cation/Qualifiers -4473 -4473 -1383 c 1329 g 859 t 2.25e-80 Matches: S23 41.068 Conservative: 54.678 Mismatches: 523 64.678 Mismatches: 536 Gaps: 4473	Ş 5			9 (1-4473	-883-2 (1-690) x	à	
RENCE 1 (bases 1 to 4473) FIRORS Bennett, C.Frank., Lipton, A. and Witters, L.M. FIRORS Bennett, C.Frank., Lipton, A. and Witters, L.M. FIROR Bennett, C.Frank., Lipton, A. and Witters, L.M. FIROR Patent, US 5968748-A 1 19-OCT-1999; FORT Location/Qualifiers FORT FORT FORT SOURCE 14473 FORT SOURCE FORT SOURC	, Q D Q			447 523 .ve: 5 3: 22 3: 736	2.25e-8 2418.00 41.06% 40.67% 64.67%	Allgnment Pred. No. Score: Percent S Best Loca Query Mat DB:	
EFERENCE 1 (bases 1 to 4473) AUTHORS Bennett, C. Frank., Lipton, A. and Witters, L.M. TITLE Antisense oligonuclectide modulation of human HER-2 expression JOURNAL Patent: US 5968748-A 1 19-OCT-1999; EATURES Location/Qualifiers 1. 4473	Qy :			9	/organism=""" 902 a 1383 c	BASE COUN	
	Db Qy	• •	2 express	itters,L.M. ion of human HE 9;		REFERENCE AUTHORS TITLE JOURNAL FEATURES	

Qy 298 Db 1009 Qy 318 Db 1069 Qy 329 Qy 329 Db 1189 Qy 329 Db 1249 Qy 329 Db 1369 Qy 329 Db 1429 Db 1429 Db 1429 Db 1549 Qy 329 Db 1569 Db 1729 Db 1789 Qy 329 Db 1789 Qy 329 Db 1789 Db 1789 Qy 329 Db 1789 Qy 329 Db 1789 Db 1789 Qy 329 Db 1849 Qy 329 Db 1849			
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ğ	1969	CGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGAT 2	2028
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ğ	2089	GACAAGGGCTGCCCCCCCGAGCAGAGAGAGCCCAGCCCTCTGACGTCCATCATCTCTGCGGTG 2	2148
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ğ	3049	TGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGC 3	108

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	ILT 13 7390	3943	551	531 3889	3829	511	6	9	3709	47	- - υ	3589	43	411 3529	3469	391	3409	4 . (υ · U	8	ء ند ا ند	330	3169	329	3109	329	
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Oy 258 GlnCysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPhe 277	Db 829 GTCTGTGCCGGTGCCTGCCCGCTGCAAGGGGCCACTGACTG		Op 218 CystysGlySerArqCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArqThr 237	198 LeuAlaLeuThrLeuIleAspThrAsnArgSerArgAlaCysHlsProCysSerProMet 21		589 GAGCTGCAGCCTTCGAAGGCCTCACAGAGATCTTGAAAGGGAGGG	Oy 158 GluLeuGlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsn 177	The remorphism of the control of the	469 CTGCGGATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGCTAGAC	118 LeuArgIleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAsp	Db 409 GAGGTGCAGGGCTACGTGCTCATCACAACTAAGTGAGGCAGGTCCCACTGCAGAGG 468	Oy 98 GluValGlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValDroLeuGlnArg 117	349 AACCTGGAACTCACCTACCTGCCCACCATGCCTGTCCTTCCT	78 AsnieuGluieuThrTvrieuDroThrAsnAlaSerieuSerbheieuGlnAsnTieGln 97	Qy 58 ProGluThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGly 77 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	222	38 GlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSer 57	178 GAGCTGGCGGCCTTGTGCCGCTGGGGGCTCCTCCTCGCCCTCTTGCCCCCC	18 PheLeuPheLeuLeuPhePheTrpLeuAspAr	Db 118 CGCCCCTCCCAGCCGGGTCCAGCCGGAGCCATGGGGGCCGGAGCCGCAGTGAGCACCATG 177	Qy 2 ArgAlaAlaProLeuLeuLeuAlaArgAlaAlaSerLeuSerLeuGly 17	390 (1-4	64.67% Indels: 6 Gaps:	Pred. No.: 2.25e-80 Length: 4473 Score: 2418.00 Matches: 523 Percent Similarity: 41.06% Conservative: 5 Best Local Similarity: 40.67% Mismatches: 22	ment Scores:	BASE COUNT 902 a 1383 c 1329 g 859 t ORIGIN	AL Patent US 6287569-A 26 11-SEP-2001; S Location/Qualifiers urce 1. 4473	
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69 CGCTGCCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGAT	1909 CCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTTCCCCTTCTGCGTGGCC 1968	1849 CACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGA 1908 329 329	329 329	1789 GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCCAGGGAGTATGTGAATGCCAGG 1848	CACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAG	9	329 329 339 329 329 329 329 329 329 329	1609 ACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAAC 1668	329 329	AGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGCTTCGTGCAC	1489 GGCGCCTACTCGCTGACCCTGCAAGGGCTGGGGCTGGGGGCTGGGGGCTGCGCTCACTG 1548		29 CTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGGACGAATTCTGCACAAT	329 329	1369 GTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGC 1428	329 329	1309 GAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG	329 329	GCCAATATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCG	OCCUPATION AND AND AND AND AND AND AND AND AND AN	1100 CCCCCAPTECACCCCCAPTECACCCCCACTECACCACCACCACCACCACCACCACCACCACCACCACCAC	AACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGT		318 CysProTyrAsnTyrLeuSerThrAspValGlySer	TTTGAGTCCATGCCCAATCCCGAGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCC	298 PheGluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAla 317	278 AsnHisSerGlyIleCysGluLeuHiSCysProAlaLeuValThrTyrAsnThrAspThr 297	

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3108	3049 TGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGC	В
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329	329	Qy
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2448	2389 TGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAC	8
329	329	Qγ
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329	329	80
2328	2269 CCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACG	망
329	329	γQ
2268	2209 CAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAG	₽
329	329	δ
2208	2149 GTTGGCATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGG	밁
329	329	8
2148	2089 GACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCATCTCTGCGGTG	망
329	329	9
2088	2029 GAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTCCT	В
329	329	γ

RESULT 14 HSERB2R LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISN	ОУ	Ф	Qy Db	Qу	Qy Db	Qу	Qу	Ωy	Qу	Оy	Qy Db	Db Qy	ОУ	Db .	Qy	Дb
T 14 2R SION ON SION PDS	551 3943	531 3889	511 3829	491 3769	47 <u>1</u> 3709	451 3649	431 3589	411 3529	391 3469	371 3409	351 3349	331 3289	330 3229	3169		3109
HSERB2R HSERB2R HUMAN C'erb-B-2 mRNA. 4473 bp mRNA linear PRI 30-MAR-1995 HUMAN C'erb-B-2 mRNA. x03363.1 GI:31197 cell surface glycoprotein; cellular oncogene; erB-2 cellular; glycoprotein; growth factor receptor; kinase; neu cellular oncogene; transmembrane protein; tyrosine kinase. Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4473)	AlaArgSerProSerPro 556	GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProAlaAlaAlaAlaPro 550 .	AsnLeuTyrTypTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLys 530	ProGlnGlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAsp 510	GlyValValLySASpValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThr 490 illiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	AlaAlaArgProAlaGlyAlaThrLeuGluArgAlaLysThrLeuSerProGlyLysAsn 470	TyrValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuPro 450 \	ProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlu 430	GlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal 410	GluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 390 	LeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSer 370 '	AlaGlyGlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAsp 350	GATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCCTGCCCCGGGC 3288	CCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTG 3228	3	ATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG

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2 (bases 1, Nikitin, A.Yu. and Rajewsky, Papewalis, J., Nikitin, at amino acid codon (
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Similarity of protein encoded by the human c-erb-B-2 gene epidermal growth factor receptor Nature 319 (6050), 230-234 (1986)
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MLRHLYOGCOVVOGNLELTYLPTNASLSFLODIOQEVOGYVLIAHNQVROVPLORLRIV
RGTOLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELOLRSLTEILKGGVLIQRNDQ
CCYQDTILWKOIFHKNNOLALTLIDTNNSRACHPCSPWCKGSRCWGESSDCOSLTRT
VCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALYTYNT
VCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALYTYNT
VCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHROBETAEDGTQRCEKC
SKPCARVCYGLGMEHLREVRAYTSANIQEFAGCKIFGSLAFLLESFDGDBASVATAPL
OPEQLQVFETLEEITGYLY 15AWPDSLPDLSVFQNLQVIRGRILHNARPEDECVGEG
LACHQLCARGLCWGFGCTCVWCSQFLRGQECVEECRVLQGLFREXVNNARHCLFCHPE
CQPQNGSVTCFGFBADQCVACAHYKDPPFCVARCPSGYKDLSYMPIWFPDEECACQ
PCPINCTHSCVDLDDKGCPADGRASPLTS ISAVVGILLVVVLGVVFGILIKRRQQKI
RKYTMRRLLGETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWI
PDGBMVKIPVAIKVLRENTSPKANKEILDEAVYWAGGVGSFVSRELGICLTSTYQLVT

PDGGRWKIPVAIKVLRENTSPKANKEILDEAVYWAGGVGSFVSRELGICLTSTYQLVT
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DLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVR
PQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAA
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NHVK ITDFGLARLDDIDETEYHADGGKVPIKWALESILRRFETHQSDVWSYGVTVWE
LMTFGAKPYDGIPAREIDDLLEKGERLPQPPICTIDVYNIMVKCWMIDSECRPRFETE
VSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGF
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/db_xref="GI:31198"
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                                     CysLysGlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThr 237
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                                                                                                                 ValCysAlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysH1sGlu
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2869 TTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTT 2928	Db	GAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGG
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2809 GCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGG 2868	Db	CACTGCTGGGGTCCAGGGCCACCCAGTGTGTGAACTGCAGCCAGTTCCTTCGGGGCCAG
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Erickson,S. and Schwal
Methods of treatment of
conjugates
Patent: WO 0100244-A
                          Homo sapiens
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P:
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                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                     DNA
             antibody-maytansinoid
                                                                            linear
                                 Euteleostomi;
Homo.
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                      LeuAlaArgGlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeu
                         ValLeuAspAsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSerProGly 154
                                                                                                                                                                                                                 GTGCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCCTCCCCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
1170 c 1121 g 71
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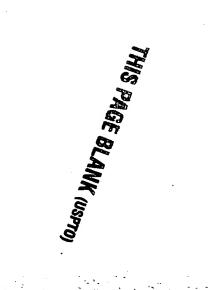
ĕ ₹	988	GTGACTGCCTGTCCCTACAACTACCTTTCTACGGAGGTGGGATCCTGCACCCTCGTCTGC 9	45 9
4	329		129
ŏ	946	CCCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGC 1	005
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õ	1006	AAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCA 1	065
¥	329	3	29
ŏ	1066	TTTGGGAGCC	125
¥	329	3	29
ਰ	1126	TTTCTGCCGGAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG	1185
~	329	3	29
ŏ	1186	CAGCTCCAAGTGTTTGAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGG 1	245
~	329	3	29
ō	1246	CCGGACAGCCTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGGACGAATT 1	305
4	329	3	29
ŏ	1306	CTGCACAATGGCGCCTACTCGCTGACCCTGCAAGGGCCTGGGCATCAGCTGGCTG	365
~	329	3	29
ō	1366	CGCTCACTGAGGGAACTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCCACCTCTGC 1	425
×	329	3	29
õ	1426	TTCGTGCACACGGTGCCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCAC 1	485
Ž	329	3	29 .
ਰ	1486	ACTGCCAACCGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCCACCAGCTGTGC 1	545
×	329	3	29
ō	1546	GCCCGAGGGCACTGCTGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTT 1	605
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ō	1606	CGGGGCCAGGAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCCAGGGAGTATGTG 1	665
Ÿ	329	3	29
ō	1666	AATGCCAGGCACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACC 1	1725
¥	329	3	129
ŏ	1726	TGTTTTGGACCGGAGGCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT	1785
٧	329		129
ō	1786	TGCGTGGCCCGCTGCCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCCATCTGGAAG 1	845
Ÿ	329	3	29
õ	1846	TTTCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCCACTCCTGTGTG 1	905
¥	329	3	29
σ	1906	GACCTGGATGACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCC	965

329 .		329	Qy	_
3045	CCAGCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGG	2986	Db	
329		329	Qy	
2985	TTCTCCCGCATGGCCAGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGC	2926	Db	
329		329	Qy	-
2925	GTCAAATGTTGGATGATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAA	2866	Дb	
329		329	Qy	
2865	GAAAAGGGGGGGGCGCCTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATG	2806	DЪ	
329		329	Qy	
2805	ATGACTTTTGGGGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTG	2746	DЬ	
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2745	CGCCGGCGGTTCACCCACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTG	2686	DЬ	•
329		329	Qy	
2685	GAGTACCATGCAGATGGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTC	2626	DЬ	
329		329	Оу	
2625	CCCAACCATGTCAAAATTACAGACTTCGGGCTGGCTGGCT	2566	дь	
329		329	Qy	
2565	CTGGAGGATGTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGT	2506	Db	
329		329	Qy	
2505	CGCCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTAC	2446	ДD	
329		329	Ωу	
2445	CTGGTGACACAGCTTATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGA	2386	Db	
329	`	329	Оу	
2385	GGTGTGGGCTCCCCATATGTCTCCCGCCTTCTGGGCATCTGCCCTGACATCCACGGTGCAG	2326	dd '	
329		329	Оу	
2325	AGGGAAAACACATCCCCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCT	2266	Db	
329		329	Qy	
2265	AAGGGCATCTGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTG	2206	Db	_
329		329	Оу	
2205	AAAGAGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTTGGCACAGTCTAC	2146	Db	
329		329	Qy	
2145	CTGGTGGAGCCGCTGACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTG	2086	Db	
329		329	Qy	
2085	AAGCGACGGCAGCAGAAGATCCGGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAG	2026	рb	
329		329	Qy	
2025	TCTGCGGTGGTTGGCATTCTGCTGGTCGTCGTGGTCTTTGGGGGTCTTTTGGGATCCTCATC	1966	Db	
329		329	Оу	

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                                                                                                                                                                                                                                                                                                   GlyLysAsnGlyValValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGlu 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProThrValProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerPro 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGlyAspLeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeu 367
                                                                                                                                                                                       TACTTGACACCCCAGGGAGGAGCTGCCCCTCAGCCCCACCCTCCTGCCTTCAGCCCA 3645
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ProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArgAlaLysThrLeuSerPro 467
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                                                                                          GCCTTCGACAACCTCTATTACTGGGACCAGGACCCACCAGAGCGGGGGGGCTCCACCCAGC 3705
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Search completed: May 8, 2003, 14:16:48 Job time: 4411 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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3739
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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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10 US-09-811-183-3
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10 US-09-811-115-3
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255	373.5	441	648.5	673	673	673	674	684	697	704.5	713.5	717	721	721	721	893	1182.	1182	1182	1183	1183	1183	1183	1183	1367.5
6.8	10.0	11.8	17.3	18.0	18.0	18.0	18.0	18.3	18.6	18.8	19.1	19.2	19.3	19.3	19.3		31.6	:	31.6	31.6	31.6	31.6	31.6	31.6	36.6
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US-10-172-620-17	US-09-847-185-2	US-09-821-883-20	US-09-925-301-1232	US-09-800-016-1	US-09-821-883-18	US-09-792-793A-15	US-09-923-246-114	US-09-783-708-1	US-10-172-620-16	US-09-867-521-2	us-09-940-101-4	US-10-102-806-583	US-09-940-101-2	US-09-725-433-2	US-10-172-620-18	US-09-441-411-9	US-09-821-883-29	US-09-821-883-27	US-09-821-883-25	US-09-930-125-11	US-09-930-125-10	US-09-930-125-8	US-09-930-125-9	US-09-854-356-4	US-09-854-356-8
	2, P		123	۲,	Sequence 18, Appl	Έ	Sequence 114, App	Sequence 1, Appli	6	2	~	583,	•	Sequence 2, Appli	Sequence 18, Appl	Sequence 9, Appli	Sequence 29, Appl	Sequence 27, Appl	Sequence 25, Appil	11,	Sequence 10, Appl	Sequence 8, Appli	Sequence 9, Appli	Sequence 4, Appli	Sequence 8, Appli

ALIGNMENTS

	240	Qy 181 CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA	
	180	Db 121 VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQL	
	180	_ [
	120	Db 61 HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI	
	120		
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	. 09	Qy 1 MRAAPLLLARAASLSLGFLFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPET	
0;	Gaps	Hest Local Similarity 100,0%; Fred. NO. 4e-212; Matches 690; Conservative 0; Mismatches 0; Indels 0; Ga	
	•	100.0%;	
		US-09-821-883-2	
		; OTHER INFORMATION: HER500-hGM-CSF construct	
		; ORGANISM: ATTITICIAL Sequence ; FEATURE:	
		TYPE: PRT	
		; LENGTH: 690	
		N	
		; SOFTWARE: FastSEQ for Windows Version 4.0	
		; NUMBER OF SEQ ID NOS: 30	
		PRIOR FILING DATE: 2000-03-30	
		PRIOR APPLICATION NUMBER: US 60/193,504	
		; CURRENT FILING DATE: 2001-03-30	
٠		TILE REFERENCE: 7030 TOVERS TIS 100 /821 R83	
•		; TITLE OF INVENTION: Cell-Based Immunotherapy	
		; TITLE OF INVENTION: Compositions and Methods for Dendritic	
		; APPLICANT: Laus, Reiner	
		GENERAL INFORMATION:	
		; Patent No. US20020061310A1	
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APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT EPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 697
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US-09-821-883-4
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                                                                                                   Matches
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Best Local (
                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                OTHER INFORMATION: HER500*-rGM-CSF construct
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                                                 MRAAPLLLARAASLSLGFLFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPET
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                                                                                                               Similarity
                                                                                                  Conservative
                                                                                                92.9%; Score 3473.5;
91.7%; Pred. No. 1.66
tive 19; Mismatches
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                                                     Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09821883 Patent No. US20020061310A1
                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                           APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                       FEATURE:
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                                                   al Similarity
549; Conserv
                                                      Conservative
                                                                  79.5%;
                                                0;
                                                                  Score 2972; DB 10;
Pred. No. 3.6e-167;
                                                     Mismatches
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APPLICANT: VIGOVIC, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Der
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
OPRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                             Matches
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Laus, Reiner
                                                                                                                                                                                                                     LENGTH: 564
TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                        ID NO 3
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              HLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI 120
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Similarity
                                                                                                             Conservative
                                                                                                                                                                                         HER500* construct
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                                                                                                                            79.18;
98.48;
                                                                                                        Score 2957.5; DB 1v
Pred. No. 2.6e-166;
Pred. No. 2.6e-166;
                                                                                                                                         DB 10;
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APPLICANT: Gheysen, Dirk
APPLICANT: Gheysen, Dirk
APPLICANT: Gorixa Corporation
APPLICANT: Smithkline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CUBRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
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SEQ ID NO 6
LENGTH: 919
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                       Best Local
                                                                                                                                     Query Match
                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                          OTHER INFORMATION: OTHER INFORMATION:
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DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 154
                                  LPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ
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                                                                                                                       Similarity
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Pred. No. 1.7e-143;
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RESULT 6
US-09-769-508-2
US-09-769-508-2
Sequence 2, Application US/09769508
Patent No. US20020155527A1
GENERAL IMFORMATION:
APPLICANT: STUART, SUSAN G.
APPLICANT: MONAHAN, JOHN J.
APPLICANT: HANCOCK, MIRIAM E.C.
APPLICANT: CHAO, LORRINE A.
APPLICANT: BLUFORD, PETER
TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP
FILE REFERENCE: BEBHJ-111-C1
CURRENT APPLICATION NUMBER: US/09/769,508
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver
SEQ ID NO 2
LENGTH: 1255
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                                        LYTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS
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Qy 215 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 274	Qy 155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 214	95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 	Qy 35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94	Query Match 64.5%; Score 2410.5; DB 10; Length 1255; Best Local Similarity 41.2%; Pred. No. 9.1e-134; Matches 510; Conservative 0; Mismatches 2; Indels 727; Gaps	; LENGTH: 1435 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-811-123-9	SOFTWARE: FASTSEQ for Windows Version 4.0	PRIOR REFLECATION NUMBER: 09/00/330 PRIOR FILING DATE: 09/00-06-23 NUMBER OF SEO ID NOS: 11	PRIOR FILING DATE: 2000-10-05 ; PRIOR FILING DATE: 2000-10-05 ; PRIOR FILING DATE: 2000-10-05	CURRENT FILIDE DATE: 2001-03-16 CURRENT FILIDED AFE: 2001-03-16	FILE REFERENCE: GENENT. 07342 FILE CONVOCALES FILE REFERENCE: GENENT. 07342 FILE CONVOCALES FILE REFERENCE: GENENT. 07342 FILE CONVOCALES	E OF INVENTION: AUTHORS OF TREATMENT US	; APPLICANT: SHATON ETICKSON ; APPLICANT: Ralph Schwall APPLICANT: Mark Clinksonk	GENERAL INFORMATION:	; Sequence 9, Application US/09811123 ; Patent No. US2002001587A1	RESULT 7	ć		500	448 PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP 507	Db 1096 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 1155	Qy 388 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 447	Db 1036 APGAGGMVHHRHRSSSTRSGGGDLTLGLEDSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 1095	330GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA	976 FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP	330	QY 330 329 Db 916 MTFGAKPYDGIPAREIPDLLEKGERLEOPPTCTIDVYMIMVKCWMIDSECRPRFREIVSE 975
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RESULT 8 US-09-811-115-3 ; Sequence 3, Application US/09811115 ; Patent No. US20020035736A1 ; GENERAL INFORMATION: ; APPLICANT: Erickson, Sharon ; APPLICANT: Schwall, Ralph	Qy 508 AFDNLYYMDQDPPERGAPPSTEKGTPTAENPETIGLDVP 546	PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPE 	QY 388 KGLOSIPTHDPSPLQRYSEDPTVPLPSETDGYVAPLT/CSPQPEYVNQPDVRPQPPSPRRG 447	330GAGGMVHHRHRSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 	Db 976 FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP 1035	916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE	Qy 330 329	Db 856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915	Qу 330 329	Db 796 LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARXVLVKS 855	Qy 330 329	Db 736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795	Оу 330 329	Db 676 KRRQQKIRKYIMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735	Qy 330 329	Db 616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILI 675	Оу 330 329	Db 556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	330	496 TANRPEDECVGEGLACHOLCARGHCWGPGPTOCVNCSOFLRGOECVEECRVLOGLPREYV	OV 330 329	330	76 FLPESFDGDPASNTAPLOPEQLOVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI	Qy 330 329	Db 316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375	. Оу 330 329

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Best Local Similarity
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LENGTH: 1
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SOFTWARE: FastSEQ for
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PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
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CURRENT FILING DATE: 2001-03-16
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TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENENT 034A
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 1255
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SmithKline Beecham Biologicals S. TITLE OF INVENTION: HER-2/neu Fusion Proteins
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OTHER INFORMATION: fragment of the phosphorylation OTHER INFORMATION: portion (delta PD)
                                                              NAME/KEY: DOMAIN
LOCATION: (990)..(1255)
OTHER INFORMATION: phosphorylation
                                                                                                                          LOCATION: (676)..(1255)
OTHER INFORMATION: intracellular domain
                                                                                                                                                                 NAME/KEY: DOMAIN
LOCATION: (1)..(653)
OTHER INFORMATION: extracellular domain (ECD)
                                                                                                                                           NAME/KEY: DOMAIN
LOCATION: (676)...
                                 NAME/KEY: DOMAIN
LOCATION: (990)..
                                                                                                                                                                                                                                  OTHER INFORMATION: human HER-2/neu protein
                                                                                                                                                                                                                                                      FEATURE:
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Corixa Corporation
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               domain, preferred
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Query Match Best Local Similarity

64.3%; 41.1%;

Score 2405.5; DB 9; Pred. No. 1.8e-133;

Length 1255

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Matches
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           --GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA
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                                           FSRMARDPQREVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP 1035
                                                                                           MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE
                                                                                                                                         PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915
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TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapien
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; Sequence 2, Application US/09930125

; Publication No. US20020193329A1
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APPLICANT:
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Foy, Teresa M.
Lodes, Michael J.
Kalos, Michael D.
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        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 6
LENGTH: 1255
                                                                                                                                                    Sequence 6, Application US/09441411
Publication No. US20030008342A1
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
                                                                                     APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
                                                           CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
TYPE: PRT
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                                                                                                                                        LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855
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                                                                                     PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915
                                                                                                                                                                                           KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ
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Pred. No. 1.8e-133;
0; Mismatches 3;
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; OTHER INFORMATION: HER300*-rGM-CSF construct
US-09-821-883-5
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US-09-821-883-5
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for I
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                 MPNPEGRYTFGASCVTACPYNYLSTDVGSAS------
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EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV 420
                                                                   MPNPEGRYTFGASCVTACPYNYLSTDVGSGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
                                                                                                                                                                    CYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%; Score 2188.5; DB 10; Length 479; 61.7%; Pred. No. 3.3e-121; tive 22; Mismatches 31; Indels 211;
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	309	0 LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTPESMPNPEGRYT	Qy 25	
	231	2 DVLRKNNQLAPVDMDTNRSRACPPCAPTCKDNHCWGESPEDCQILTGTICTSGCARCKGR	Db 17	
	249		Qy 190	
	171	YALAYLDNGDENN-TTPVTGASPGGLKELQLKSLTEILKGGVLIQKNPQLCYQDTILWK 	Qy 131 bb 112	
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	130	1 GCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDN	Qy 7	
	51	A AAWCRWGFLLALLSPGAAGTQVCTGTDMKLRLPASPETHLDMLRHLYQ	Db 4	
Ų	י ד	*34; CONSELVACIVE	. אַם	
	l .	tch 52.4%; Score 1961; DB 9; Length 1256; al Similarity 34.3%; Pred. No. 2.4e-107;	Query Ma	
		R INFORMATION: mouse HER-2/neu protein 4-356-14) US-09-85	
		NISM: Mus sp.	ORGA	
		TH: 1256	LENG	
		ARE: PatentIn Ver. 2.1	SEO ID	
		APPLICATION NUMBER: US 6U/11/,9/6 FILING DATE: 199-61-29 DOE GEO TO NOC: 26	PRIOR	
		93,48	PRIOR	
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		ion Proteins	FILE	
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		CANT: Cheever, Martin A. CANT: Gheysen, Dirk	; APPLI	
			; Patent	
		RESULT 13 US-09-854-356-14 ; Sequence 14, Application US/09854356	RESULT 1 US-09-85 ; Sequen	
		2 FLFDIPFDCWKPVQKGAPPPPAHHHHHH 479	Db 45	
		1 FLLVIPFDCWEPVQEGAPPPРАААННННН 690	Оу 66	
	451	2 TCVQTRLKLYKQGLRGNLTKLNGALTMIASHYQTNCPPTPETDCEIEVTTFEDFIKNLKG	Db 39	
	660		Qу 601	
	391	AAPTRSPNPVTRPWKHVDAIKEALSLLNDMRALENEKNEDVDIII	Db 339	
	600	1 LGLDVPAAAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEP	Оу 54	
•	338	5	Db 33	
	540	GAVENPEYLTPQGGAAPQPHPPPAFSP.	Qy 481	
	334	12IIN	Db 33	
	480	APLTCSPQPE	Qy 421	
	331	2	Db 332	

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RESULT 14
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                                                                                     PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP 422
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                                                                                                                                         LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA 482
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                                            LDVP 1255
                                                                                                                              LACSPQPEYVNQPEVRPQSPLTPEGPPPPIRPAGATLERPKTLSPGKNGVVKDVFAFGGA
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                                                                LDVP 546
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PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 118
LENGTH: 1260
TYPE: PRI
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APPLICANT: TERMAN, DAVID S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.2%; Score 1950.5; DB 9; Best Local Similarity 34.1%; Pred. No. 9.8e-107; Matches 433; Conservative 24; Mismatches 72;
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CURRENT FILING DATE: 2002-01-14
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  710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 RHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQ 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITGYLYISAWPDSLRDLSVFQNLRIIRGRILHDGAYSLTLQGLGIHSLGLRSLRELGSGL 469
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AMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKAN 769
                                                                                        EQRASPVTFIIATVEGVLLFLILVVVVGILIKRRRQKIRKYTMRRLLQETELVEPLTPSG
                                                                                                                                                                                   AACAHYKDSSSCVARCPSGVKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPA
                                                                                                                                                                                                                                                                                                                                                             ALIHRNAHLCFVHTVPWDQLFRNPHQALLHSGNRPEEDLCVSSGLVCNSLCAHGHCWGPG
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Qy 330 329	_	KEY: DOMAIN
Db 832 KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEVHADGGKVPIKWMA 891		
Оу 330 329	٠.	0
Db 772 AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNWCVQIA 831		NAME/KEY: DOMAIN LOCATION: (677)(1256)
Оу 330 329		: LOCATION: (1)(654) : OTHER INFORMATION: extracellular domain (ECD)
Db 712 QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE 771		
Qy 330 329		ORGANI
Db 652 VTFIIATVEGVLLFLILVVVVGILIKRRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQA 711		LENGTH:
Оу 330 329		SOFTWARE: PatentIn Ver
Db 592 KDSSSCVARCPSGVKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASP 651		PRIOR FILING DATE: 1999-01-29 NUMBER OF SEO ID NOS: 26
Qy 330 329		PRIOR FILING DATE: 2000-01-20 PRIOR ADDITION NUMBER: (1S
Db 532 CSHFLRGQECVEECRVWKGLPREYVSDKRCLPCHPECQPQNSSETCFGSEADQCAACAHY 591		FILING DATE: 2001-05-09
Qy 330 329		REFERENCE: 014058-009810PC
Db 472 NAHLCFYHTYPWDQLFRNPHQALLHSGNRPEEDCGLEGLYCNSLCAHGHCWGPGPTQCVN 531		APPLICANT: SmithKilne Beecham Biologicals S. A. TITLE OF INVENTION: HER-2/new Fusion Proteins
Qy 330 329	· . <u>.</u> .	
Db 412 YISAWPDSLRDLSVFQNLRIIRGRILHDGAYSLTLQGLGIHSLGLRSLRELGSGLALIHR 471		GENERAL INFORMATION: APPLICANT: Cheever, Martin A.
Qy 330 329		ence 2,
Db 352 RGARAITSDNVQEFDGCKKIFGSLAFLPESFDGDPSSGIAPLRPEQLQVFETLEEITGYL 411		RESULT 15 US-09-854-356-2
Qy 330 329	•	
		OY 537 NPEYLGLDVP 546 Db 1250 NPEYLGLDVP 1259
Qy 310 FGASCYTACPYNYLSTDYGS 329		DD 1190 FAFGGAVENPEYLVPREGTASPPHPSPAFSPAFDNLYYWDQNSSEQGPPPSNFEGTPTAE 1249
QY 230 LETDCCHEQCANGCTGERNSDCLANCHERNSGICELHCERALVITATITEESMENEGERIT 393		477 FAFGGAVENPEYLTPOGGAAPQPHPPPAFSPAFDNLYYWDQDPDERGAPPSTFKGTPTAE
172 DVFRKNNQLAPVDIDTNRSRACPPCAPACKDNHCWGESPEDCQTLTGTICTSGCARCKGR		Db 1130 DGYVAPLACSPQPEYVNQSEVQPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDV 1189
DIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGP	· :	
Db 112 YALAVLDNRDPQDNVAASTPGRTPEGLRELQLRSLTEILKGGVLIRGNPQLCYQDMVLMK 171		The statement of the st
Qy 131 YALAVLDNGDPLNNTTPVT-GASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWK 189	:	TOTO TREEDED TO TOTO TOTO TOTO TOTO TOTO TOTO T
Db 52 GCQVVQGNLELIYLDETNASLSELQDIQEVQGYVLIAHNQVKRVDLQRLRIVRGTQLFEDN 130	- 	330GAGGMVHHRHRSSSTRSGGGDLTLGLE
4 AAWCKWGELLAULPPGLAGTQVCTGTDMKLKLPASPETHLDMLKHLYQ		Db 950 PICTIDVYMIMVKCWMIDSECRPRERELVSEESRMARDPQREVVIQNEDLGPSSPMDSTF 1009
11 AASLSLGFLFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQ	•	ОУ 330 329
Matches 433; conservative 21; mismatches /U; indeis /4U; caps		Db 890 PIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQP 949
atch 52.1%; Score 1948; DB 9; Length 1250; cal Similarity 34.3%; Pred. 1.4e-106;		Оу 330 329
33012	73	Db 830 WCVQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKV 889
THER INFORMATION: Iragment of the phosphorylation domain, preferred OTHER INFORMATION: portion (delta PD)		Оу 330 329
ION: (991)(1049)		Db 770 KEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLN 829
~ ~	٠.	ОУ 330 329

B	892	892 LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 951	
Ŷ	330	329	
B	952	VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPSSPMDSTFYRSLLE 1011	
QY.	330	330GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEA 362	
В	1012	DDDMGDLVDAEEYLVPQQGFFSPDPTPGTGSTAHRRHRSSSTRSGGGELTLGLEPSEEGP 1071	
δ	363	PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP 422	
8	1072	PRSPLAPSEGAGSDYFDGDLAMGYTKGLQSLSPHDLSPLQRYSEDPTLPLPPETDGYVAP 1131	
Ŷ	423	LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA 482	
B	1132	LACSPQPEYVNQSEVQPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFAFGGA 1191	
Ŷ	483	VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG 542	
₽	1192	VENPEYLVPREGTASPPHPSPAFSPAFDNLYYWDQNSSEQGPPPSNFEGTPTAENPEYLG 1251	
ν	543	543 LDVP 546	
망	1252	LDVP 1255	

Search completed: April 28, 2003, 13:44:03 Job time : 40.3846 secs

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Result
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Maximum Match 100%
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US-09-146-283-4
US-09-344-195-4
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                                             Query Match
Best Local S
Matches 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cheever, Martin A. APPLICANT: Disis, Mary L.
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	10, Appl	8, Appli	142, App	•	142, App	142, App	142, App	•	144, App	144, App	144, App	144, App	4, Appli	4, Appli	9, Appli	4, Appli	5183884	z, Appii

ALIGNMENTS

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TELEX: 3723836 SEEDANBERI
INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
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APPLICATION UMBER: US/08,
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
                                                                                                                                                                                                                     NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
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PAPELICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 3723836 SEEDANBERRY
 Local Similarity .
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GY: linear
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Best Local Similarity 41.1%;
Matches 509; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/414,417B FILING DATE: 31-MAR-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Sharkey, Richard G. REGISTRATION NUMBER: 32,629 REFERENCE/DOCKET NUMBER: 920010.446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                    215 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                       136 GLRELQLRSLTEILKGGYLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHPC
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   LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS-----
                                      SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
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Pred. No. 4.8e-179;
0; Mismatches 3;
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US-08-486-348A-68
(Sequence 68, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
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Matches 509
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APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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STATE: Washing
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les 509; Conserv
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TELEFAX: (206) 682-603 INFORMATION FOR SEQ ID NO: FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY_AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE_FOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC POS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS CORRESPONDENCE ADDRESS: LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 485 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375 6300 Columbia 64.3%; ilarity 41.1%; Conservative (206) 622-4900 206) 682-6031 Seed and Berry LLP 00 Columbia Center, US/08/486,348A 68: Score 2405.5; DB 2; Pred. No. 4.8e-179; 0; Mismatches 3; 920010.448C6 701 Fifth Avenue Version # Length Gaps . 3291 255 274 195 214 ;

RESULT 4 US-08-625-101-2 Sequence 2, Application US/08625101 Patent No. 5869445 GENERAL INFORMATION: APPLICANT: Cheever, Martin A. APPLICANT: Cheever, Martin A. APPLICANT: Disis, Mary L. TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu TITLE OF INVENTION: ONCOGENE IS ASSOCIATED NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104-7092 COMPUTER REACABLE FORM: MEDIUM TYPE: Floppy disk	330 916 330 976 330 1036 388 .1096 448 1156	
Db 376 FLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 435 Qy 330	Qy	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/625,101 FILING DATE: 01-APR-1996 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Sharkey, Richard G. REGISTRATION NUMBER: 32,629 REGISTRATION INFORMATION: TELEPHONE: (206) 622-4900 TELEFAX: (206) 622-6900 TELEFAX: (206) 622-6

1;

TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 TELEPAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 68:	ORNEY/AGENT INFORMATION: AME: Sharkey, Richard G. EGISTRATION NUMBER: 32,629	; APPLICATION NUMBER: US/08/468,545B; FILING DATE: 06-JUN-1995; CLASSIFICATION: 424	Rel ATA:	STE	PUTER	COUNTRY: US	Seattle Concer, for them.	CURRESFONDENCE ADDRESS: STREET: 6300 Columbia Conter 701 Fifth Avenue	ENCES:	OF INVENTION: IMMUNE REACTIVITY TO HOF INVENTION: FOR DIAGNOSIS AND TREACTIVITY	CANT: Cheever, Martin A.	RMATION:	; Sequence 68, Application US/08468545B	3	DO 1216 AFUNLYYMDQUFFERGAFFSTENGTPTAENPEXIGLDVP 1254	508 AFUNLYYMOQDPPERGAIPSTFKGTPTAENPEYLGLDVP 546	1130	446 PLPANKPAGAYLEKANILSPOKNIGVKUVFARGGAVEDPYKLTPQGGAAPQPHPPPAFSP 5	1096 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG	1036 APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA		976 FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP	Db 916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975	ОУ 330 329	Db 856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915	330	The 706 i upot maddet i dendet i dendet i mad motavoneri edniet i dendet i vacanti urc. Oss	736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 7	330 32
Db 856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915 Qy 330 329 Db 916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975	330	QY 330 329 QY 370	Db 736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795	Qy 330 329	Db 676 KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735	Qy 330 329	Db 616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI 675	Qy 330 329	Db 556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	Qy 330 329	Db 496 TANRPEDECVGEGLACHQLCARCHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 555	Qy . 330 329	Db 436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495	Qy 330 329	Db 376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 435	Оу 330 329.	Db 316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375	Оу 330 329	Qy 275 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS 329	QY 215 SPMCKOSRCWGESSEDCQSJJHTIVCAGGCARCKGPLPTDCCHEQCAAGCTGPRHSDCLAC 2/4	136 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC	Qy 155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 214	76 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVYGASPG 13	95 DIOEVOGYVLIAHNOVBOVPIORLRIVBGTOLFEDNYALAVLDNGDPLNNTTPVTGASPG	Qy 35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94	Matc)	h 64.3%;	; TOPOLOGY: linear US-08-468-545B-68	ENCE CHAR NGTH: 12 PE: amin

	_	LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94	Qy 35 LARGAASTQVCTG
388 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 44	 Oy	vative 0; Mismatches 3; Indels 727; Gaps 1;	Macches 509; Conser
330GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 38	Db Oy	h 1255;	Query Match Best Local Similarity
ESRMARDPQREVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP	. Db	protein	E:
330 32	Qy		Y:
916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCMMIDSECRPRERELVSE 97	Db	ISTICS:	SEQUENCE CHARACTERISTICS: LENGTH: 1255 amino aci
330 320	Qy	248-7100 ID NO: 2:	TELEFAX: (617) 248-7100 : INFORMATION FOR SEO ID NO: 2:
856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 91	dα	Z. ;	TELECOMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
330 321	Оу	BER: 27,829	97
796 LYTQLMPYGCLLDHYRENRGRLGSQDLLNWCMQIAKGMSYLEDYRLYHRDLAARNYLYKS 85	. ab	ORMATION:	P
330 320	Qy	IMBER: 07/831,967	APPLICATION NUMBER:
736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 79	. Db	424 DATA:	CLASSIFICATION: 424
330 321	Qy	ER: US/08/356,786	APPLICATION NUMBER:
676 KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 73:	dd	PatentIn Release #1.0, Version #1.25	SOFTWARE: Patentin Rel
330 32		C compatible	COMPUTER: IBM P
616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI 67	рь	FORM:	= F
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556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 61	Db		Z B
330 32:	Qy	Exchange Place. 53 State Street	ADDRESSEE: Edmund
496 TANRPEDECYGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECYEECRYLQGLPREYV 55	Db	RESS:	NUMBER OF SEQUENCES: 1
330 32	Qy	-	; TITLE OF INVENTION:
436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 499	Db		APPLICANT: Houston, L.
330	Qy	James S.	3
376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 43	Db	. APPLICATION US/U8336/86	; sequence 2, Application; Patent No. 5877305
330 32	Qy		
316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 37	Db		
330 32	Qy	AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254	Db 1216 AFDNLYYWDQDPP
256 LHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 31:	Db	ERGAPPSTFKGTPTAENPEYLGLDVP 546	QY 508 AFDNLYYWDQDPP
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SPMCKGSRCWGESSEDCOSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC	Db		448
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95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 15	. Qy	FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP 1035	Db 976 FSRMARDPQRFVV
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US-08-466-680B-68
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                                                                                                                                                                                                                                                                                                                        Query Match 64.3%;
Best Local Similarity 41.1%;
Matches 509; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sharkey, Richard G
REGISTION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cheever, Martin A. APPLICANT: Disis, Mary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1096 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 1155
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                                                                                                                           196
                              275
                                                                                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                           95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                              LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS-----
                                                                                 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCCHEQCAAGCTGPKHSDCLAC 274
                                                                                                                                                                                            DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1255 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25 '..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/466,680B
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                                                                                                                                                                                                                                                                                                                        Score 2405.5; DB 3;
Pred. No. 4.8e-179;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                        DB 3;
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                                                                                                                                                                                                                                                                                                                                                      Length 1255;
                                                              255
                              329
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RESULT 8
US-08-484-438-8
US-08-484-438-8
; Sequence 8, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
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508 AFDNLYYWDQDPDERGAPPSTFKGTPTAENPEYLGLDVP 546 	Qy Db
448 PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPOGGAAPOPHPPPAFSP 507	Qy Db
388 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 447 	Qy Db
330GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 387 	Db. 04
976 FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP 1035	Db
330 329	Qy
916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975	DЬ
330 329	Qy
856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915	DЬ
330 329	Qγ
796 LYTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855	В
330 329	Qy
736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795	DЬ
330 329	Qy
676 KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSSAFGTVY 735	р р
330 329	Qy
616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI 675	ф
330 329	Qy
556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	DЬ
330 329	Qy
496 TANRPEDECVGEGLACHQLCARCHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 555	Db
330 329	οy
436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNFHQALLH 495	DЪ
330 329	Qy
376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 435	В
330 329	Qу
316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375	ф
330 329	Qy
256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 315	Дb

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Best Local Similarity
Matches 509; Conserv
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: ur
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                                                                                                                155 GLRELQLRSLTEILKGGYLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC
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                                                   215 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
275 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS-----
                                  196
                                                                                               136 GLRELQLRSLTEILKGGYLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC
                                                                                                                                                                                                                             LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                               95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               76 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/323,442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                 Conservative
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Hellstr m, Karl E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plowman, Gregory D.
Culouscou, Jean-Michel
                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENNIE
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l, Clay B.
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Pred. No. 1.8e-177;
0; Mismatches 2;
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                                                                                                                               214
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 329
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	AFDNLYYWDQDPPERGAPPSTEKGTPTVAENPEY-GLDVP 1254	1216	Db
	NPEYLGLDVP 5	508	Qy
1215		1156	D
507	LPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP 5	448	Qy
1155	KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG	1096	DЬ
147	Δ.	388	Qy
1095		1036	Дb
387	GAGGMYHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 3	330	Qy
1035	FSRMARDPQREVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP 1	976	Db
329	3	330	Qy
975 '	MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 9	916	DЬ
329	3	330	Qy
915	VWSYGVTVWEL	856	ФФ
329	3	330	Qy
- LA	LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 8	796	Db
329	3	330	Qy
vo	KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 7	736	Дb
329	3	. 330	Qy
735	KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 7	676	Db
329	3	330	Qy
675	FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILI 6	616	Дb
329	3	330	Qγ
515	NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 6	556	фd
329	3	. 330	Qy
555	TANRPEDECVGEGLACHQLCARRALLGSGPTQCVNCSQFLRGQECVEECRVLQGLPREYV 5	496	Дb
329	3	330	Qy
195	LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 4	436	Db
329		330	Qy
135	FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 4	376	Db
329	3	330	Оу
375	PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANTQEFAGCKKIFGSLA 3	316	d Db
329	3	330	Qy
315		256	Db

US-09-146-283-4
US-09-146-283-4
: Sequence 4, Application US/09146283
: Patent No. 5976546
: GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: p:
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                  314
                                                                                                                                                                                                                                                                                                                   155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHPC 214
                                  374
                                                                                                                                 335
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                                                                                                                                                                                                                                                                                                                                                                                   95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                16 LPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Judge, Linda R. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09
FILING DATE: 03-SEPT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSGAGGM 334
                               LAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRG 433
                                                                                                                                                                                                                                                                 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 274
                                                                                                                                                                                                                                                                                                GLRELQLRSLTEILKGGYLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 195
                                                                                                                                                                                                                                                                                                                                                                  DIGEVOGYVLIAHNOVROVPLORLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 135
                                                                 ----SDVFDGD----
                                                                                               VCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGS
                                                                                                                                 VHHRHRSSSTRSGGGD----
                                                                                                                                                                LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCT--L 313
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Ruegg, Curtis L.
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PC-DOS/MS-DOS
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Pred. No. 3
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-DPSPLQRYSEDP----
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RESULT 10
US-08-579-823A-4
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                                                                                                                                              TELEFAX: 650-324-0960
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APPLICANT:
                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,
                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                              ORIGINAL SOURCE:
                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 03-DEC
                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                  ORGANISM:
                                                                             TOPOLOGY:
                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM
                                                                                                            LENGTH:
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SYSTEM: PC-DOS/MS-DOS
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GM-CSF-Her-2 fusion protein; Fig.
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RESULT 11
US-09-344-195-4
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                                                                                                             Sequence 4, Application Patent No. 6210662 GENERAL INFORMATION:
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   Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                              APPLICANT: Laus, Reiner
                                                                                                                                                                                                                                                 EN----PEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGA-PPSTF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                          DQCVACAHYKDPPFCVA---RCPSGVKPDLSYMPIW-KFPDEEGACQPCPINCTHSCVDL
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ADDRESS:
: Dehlinger
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                                                                                                                                             US/09344195
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                              275 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSGAGGM
                                                                                                                                                                                                                                                                                                            215
                                                                                                                                                                                                                                                                                                                                            136
               434 RILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFKNPHQAL
                                                                                                                                                                                                              256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCT--L
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                                                                                                                                                                                                                                                                                                                                                                                                         76 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG
                                                                                                                                                                                                                                                                                                                                                                                                                                         95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PETENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig.
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                             LAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRG
                                                                                                                                                                            VHHRHRSSSTRSGGGD------LTLGLEPSEEEAPRSPLAPSEGAG-----
                                                                                                                                                                                                                                                                                             SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                                                                                                                                                         ---SDVFDGD---
                                                                                                                                             VCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGS
                                                                                                                                                                                                                                                                              SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                             -------LGMGAA-KGLQSL-------PTH----DPSPLQRYSEDP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 7636-0010.21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2224; DB 4;
Pred. No. 3.6e-165;
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US-09-630-155-2
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Patent No. 6414130
GENERAL INFORMATION:
APPLICANT: Doherty, Jon1 Kr1
TITLE OF INVENTION: HER-2 BI
                                                                                                   Query Match
                                                                   Matches
                                                                                                                                                                                                                                                    TELEFAX: 206 628-7699
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                               35
                                                                 Local Similarity 77.1 ies 318; Conservative
 16
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ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 206 628-7621
                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
               LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94
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LPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ
                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        NAME: Davison, Barry L.
REGISTRATION NUMBER: 47,309
REFERENCE/DOCKET NUMBER: 49
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/630,155 FILING DATE: 16-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: PC compatible
                                                                                                                                                                                                                                      LENGTH: 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Windows95
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                                                                                                                                                                                    unknown
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                                                                   9
                                                                 Score 1607; DB 4;
Pred. No. 2e-117;
9; Mismatches 55;
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                                                                                               Length 419;
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US-08-422-108-1
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                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/354
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M
REGISTRATION NUMBER: 00,00
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WinPatin (Ger
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hudziak, Robert M. APPLICANT: Shepard, H. Michael APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ullrich, Axel
TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 GPAHPVLSFLRPSWDLVSAFYSLPLAPL-SPTSVPISPVSVGRGPD----PD 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 LPTHDPSPLORYSED-----PTVPLPSETDGYVAPLTCSPQPEYVNQPD 436
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                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/3
FILING DATE: 13-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                 TELEX:
                                                                               TELEFAX:
                                                                                                 TELEPHONE:
                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 15-AP
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 14-Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              South San Francisco
                                                                 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
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                                                                                   415/952-9881
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Best Local Similarity
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                         FILING DATE: 15-APR-PRIOR APPLICATION DATA:
                                                                     PRIOR APPLICATION DATA:
                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 14-Apr-
                                                                                                                                                                                                                  SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                          APPLICATION NUMBER:
                                                                                          FILING DATE:
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                                                                                                       APPLICATION NUMBER:
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              NUMBER:
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19-MAY-1989
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Sequence 69, Patent No. 5

5801005

Application US/08414417B

GENERAL INFORMATION:

APPLICANT:

Cheever, Martin A. Disis, Mary L.

TITLE OF INVENTION: TITLE OF INVENTION:

IMMUNE REACTIVITY TO HER-2/neu PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES

HER-2/neu ONCOGENE IS

ASSOCIATED

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WHICH

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP

STREET: 6300 CCITY: Seattle

6300 Columbia

Center,

701 Fifth Avenue

COUNTRY:

Washington

98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:

US/08/414,417B

Version

#1.25

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RESULT 15
US-08-414-417B-69
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Best Local :
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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                                                                  359 SFDGD------PASNTAPLO 372
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                                                                                                                                          299 QEVTAEDGTORCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPE 358
                                                                                                                                                                              341 SSSTRSGGGD-------LTLGLEPSEEEAPRSPLAPSEGAG-----SD
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US-08-414-417B-69
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INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS:
LENGTH: 580 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 95.6%;
Matches 219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2
                                                                  411
                                                                                                                                                          378 FDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDV 437
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531 QPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 579
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                    QPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546
                                                                                                                                        FDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDV 470
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Pred. No. 3.8e-84;
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Search completed: April 28, 2003, 13:43:11 Job time: 34.1923.secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                        sp_plant:*
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   149
643
655
1210
1209
478
331
1165
144
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             014256

08WYV0

09B366

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09BG76

1 09EFV5

1 09EFV5

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                                                                                                                                                           018735
Q9UK79
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Q9uk79 homo sapien
Q8r2x1 mus musculu
Q14256 homo sapien
Q8wyv0 homo sapien
Q90836 gallus gall
Q9bg66 oryctolagus
Q9bg76 mus musculu
Q9wyf5 mus musculu
Q9wyf5 mus musculu
Q9qx70 rattus norv
Q9ese0 rattus norv
Q9ese0 rattus norv
Q9bud7 homo sapien
Q9yh40 xiphophorus
Q9g144 macaca mula
Q9gsh2 gallus gall
                                                                                                                                                                                           Description
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238	247	256	56	259.5	263	270.5	272.5	•	273.5	274	289	291	323.5	331	331	341	341	362	377	395	398	407	427	515	528	543	545	809
6.4					7.0		7.3								8.9	9.1	9.1	9.7	10.1	•	10.6	•	٠	•	14.1			16.3
469	1368	1369	1362	1412	1358	2144	1418	1418	89	1749	1671	1472	1193	342	334	1717	366	138	1368	151	150	1137	141	152	146	1433	144	1328
11	13	13	13	13	13	თ	13	<u>1</u> 3	11	ۍ.	S	υı	S	S	Ŋ	σ	5	1				13	1				σ	13
Q63721	Q8UW85	Q8UW86	Q9PVZ4	Q8UW84	073798	Q9VD94	093457	Q8UW83	088459	QBT0W6	Q9NJV5	Q9U5A8	Q9Y1X8	Q26568	Q26567	Q26566	Q26569	099J91	Q23821	Q9BG65	Q9BG64	Q9W6F6	Q8VH40	Q95L10	Q8WN17	09він9	Q9MYK4	P79754
1	5	0		28uw84 paralichthy	В	a		ω	φ			5a8	Q9y1x8 ephydatia f	Q26568 schistosoma	Q26567 schistosoma	Q26566 schistosoma	Q26569 schistosoma	Q99j91 marmota mon	Q23821 caenorhabdi	Q9bg65 oryctolagus	Q9bq64 oryctolagus	. Q9w6f6 gallus gall	Q8vh40 sigmodon.hi	Q95110 equus cabal	7	anoph	Q9myk4 ovis aries.	P79754 fugu rubrip

ALIGNMENTS

					.	
335	Qy		378	330GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVF		οy
256	Db		1025	966 PRERELVAEFSRMARDPOREVVIQNEDLGPASPLDSTEYRSLLEDDDMGDLVDAEEYLVP	9	DЬ
275	Qγ		329	330	ω ω	δõ
196	рb		२ 965	906 SYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECR		Db
215	Qy		329	330	w	γ
136	рь		₹ 905	846 AARNVLVKSPNHVKITDEGLARLLDIDETEYHADGGKVPIKWMALESIPPRRETHQSDVW	œ	문
155	Qу		329	330	w	Ş
76	Db		845	786 GICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNWCVQIAKGMSYLEDVRLVHRDL	7	В
95	Qy		329	330	u u	Q
16	В		785	726 GSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLL	7	망
ω 	Qy		329	330	ພ	Qy
Matches	X 9	•	725	666 VGLVLGILIKRRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVL	60	망
uery M		. •	329	330	ω ¹³	Q
SEQU	so Dk	. •	/ 665	606 DLSFMPIWKFADEEGTCQPCPINCTHSCADLDEKGCPAEQRASPVTSIIAAVVGILLAVV	•	망
Pfan	D R	- .	329	330	w	Qy
Inte	S D R	-	605	546 LQGLPREYVKDRYCLPCHSECQPQNGSVTCFGSEADQCVACAHYKDPPFCVARCPSGVKP	L/s	밁
EMBL	DR F	٠.	329	330	ω	Qy
Dohe	RA		/ 545	486 FRNPHQALLHSANRPEEECVGEGLACYPCAHGHCWGPGPTQCVNCSQFLRGQECVEECRV	4	DЬ
	RR		329	330	w	Qy
auto	RI		485	426 ONLRVIRGRVLHDGAYSLTLQGLGISWLGLRSLRELGSGLALIHRNARLCFVHTVPWDQL	_	90
Dohe	R X		329	330	(L)	οy
DOGS	א א א		425	366 GCKKIFGSLAFLPESFDGDPASNTAPLQPEQLRVFEALEEITGYLYISAWPDSLPNLSVF	w	Вb
NCBI	2 2		329	330	ω	Qy
Euka	888		365	TOUGSCTLYCPLNNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFA	w	В
HER-	GN		329	325 TDVGS	La)	Qy
017.			3 324 3 305	265 GPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLS		р о у
09UK	A II		245	186 THRESACPPCSPACKDAHCWGASSGDCQSLTRTVCAGGCARCKGPQPTDCCHEQCAAGCT		D
ULT 2 K79	RESULT 09UK79		264	205 TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT		γo
1206	Db			126 GIPAPGAAQGGLRELQLRSLTBILKGGVLIQRSPQLCHQDTILWKDVFHKNNQLALTLID		В
494	Qy			145 TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI		QΥ
1146	Db		ш.	66 PANASLSFLQDIQEVQGYVLIAHSQVRQIFLQRLRIVRGTQLFEDNYALAVLDNGDPLEG		Db .
439	Оy			85 PTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN		γo
1086	מם		6 8	25 WLDRSVLAKELARGAASTQVCTGTDMKLRLASPETHLDMLRHLYQCCQVVQGNLEELTYL 		D Q
379	Оу	4;	- 0	The state to mindiches 44; inders (31)	אפרכוזפ	,
1026	Db		,	h 1259;	Query Best I	

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Match
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herty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner W.D.;
bmitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
bl.; AF177761; AAD56009.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QUENCE FROM N.A.

DLINE-99415951; PubMed-10485918;

herty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;

he HER-2/neu receptor tyrosine kinase gene encodes a secreted toinhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terPro; IPR000494; EGFR_L_domain.
terPro; IPR002174; Furin-like.
am; PF00757; Furin-like; 1.
am; PF01030; Recep_L_domain; 1.
aRT; SM00261; FU; 1.
QUENCE 419 AA; 45472 MW; FEC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          no sapiens (Human).
karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAY-2000 (TrEMBLrel. 13, Created)
MAR-2001 (TrEMBLrel. 16, Last sequence update)
UN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSGAGGM
                                                                                                                                                       SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                                                       GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSKACHPC
                                                                                                                                                                                                                                                                                                      POPPSPREGPLPAARPAGATLER-----AKTLSPGKNGVVKDVFAFGGAVENPEYLTPQG 493
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VHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLP
                                                                                                                               SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                                      GLRELOLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC
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                                          LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCT--L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45472 MW; FEC1BE347E2D030C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1609.5; DB 4; Length Pred. No. 6.2e-112; 7; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
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                                                                                                                                                                                                                                                                                                        135
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Best Local :
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                                                                                                                                                                                     Q14256 PRELIMINANA,
Q14256;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-orb B2/neu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8R2X1
Q8R2X1;
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR 2002) to the
EMBL; BC027008.1;
                                                                                                                           Teru 2.
C-ERB B2.
Homo sapiens (Human).
Homo sapiens (Human).
Horia; Chordata;
Horia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical 40.2 kDa protein. Mus musculus (Mouse). Eukaryota, Metazoa; Chordata; (Mammalia; Eutheria; Rodentia; (
                SEQUENCE FROM N.A.

MEDLINE-86070181; PubMed-2999974;

COUSSENS L., Yang-Feng T.L., Liao Y.C., Chen E
Seeburg P.H., Libermann T.A., Schlessinger J.,

Levinson A., Ullrich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Creat
01-JUN-2002 (TrEMBLrel. 21, Last
01-JUN-2002 (TrEMBLrel. 21, Last
                                                                                                                         NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein SEQUENCE 367 AA;
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Pred. No. 3.1e-64;
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                                                                                                                                           Craniata; Vertebrata; I Catarrhini; Hominidae;
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J., Francke Γ
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rancke U.,
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Best Local S
Matches 183
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Best Local S
Matches 165
                                                                                                           ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
Hypothetical protein.
Hypothetical protein.
SEQUENCE 412 AA; 44702 MW; 034397F
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata; Metazoa; Primates;
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SEQUENCE
                                                                                                                                                                                                   InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
                                                                                                                                                                                                                                      Submitted (NOV-2000) to the EMBL; AF318349; AAL55856.1; InterPro; IPR002048; EF-hanc
                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical PP3659.
                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 44.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sarkar F.H., Ball D.E., Li Y.W., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-94000386; PubMed-8104414;
Sarkar F.H., Ball D.E., Li Y.W., Crissman
                                                                                                                                                                               Pfam; PF00069; pkinase; Pfam; PF02757; YLP; 2.
                                                                                                                                                                                                                                                                        growth."
                                                                                                                                                                                                                                                                                             Wan D.F., Gu J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shares chromosomal location with neu Science 230:1132-1139(1985).
                                                                                                                                                                                                                                                                                    "Novel human cDNA
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8WYV0;
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hes 183;
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mes 165; Conserv
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                     GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAEN
LGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQP
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                                                                            Similarity
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llarity 100.0%;
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                                                                  Score 900.5;
Pred. No. 4.7e
6; Mismatches
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Pred. No. 5.4e-60;
0; Mismatches 0;
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                                                                                                                034397FF3F27D2BC
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Matches 160
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SEQUENCE
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MEDLINE-92123214; PubMed-1732751;

MEDLINE-92123214; PubMed-1732751;

Filickinger T.W., Maihle N.J., Kung H.-J.

"An alternatively processed mRNA from the soluble, truncated form of the receptor soluble, truncated form of the receptor."
                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                              dependent transformation. Mol. Cell. Biol. 12:883-89 EMBL; M77637; AAA48759.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gâllus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR002174; Furin-like.
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 244
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                                                                                                                                         LVLLLLLGRVALCS----AVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSN
                                                    ALTILID-TINGSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCH
                                                                                     YH-MNKTQ--
                                                                                               LFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
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NQCAAGCTGPRESDCLACRKFRDDATCKDTCPPLVLYNPTTYQMDVNPEGKYSFGATCVR
                                          PLTVLDFASNLSSCPKCHPNCTEDHCWGAGEQNCQTLTKVICAQQCSGRCRGKVPSDCCH
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                                                                                                                                                                                                                     160;
                                                                                                                                                                                                                                                                                                                 PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                                                                                              PF00757; Furin-like;
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Similarity 42.4%;
60; Conservative 5
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527 /
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. 21, Last annotation update)
precursor.
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                                                                                                                                                                                                                  Score 754.5; DB
Pred. No. 5e-48;
6; Mismatches 1
                                                                                                                                                                                                                                                             POTENTIAL.
EGF/TGF-ALPHA RECEPTOR.
; 764564ABCC095298 CRC64;
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; Galliformes; Phasianidae; Phasiani
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ligand-
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01-MAR-2001 (TrEMBLrel. 16
01-MAR-2001 (TrEMBLrel. 16
01-JUN-2002 (TrEMBLrel. 2
Epidermal growth factor r
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NON_TER
SEQUENCE
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SEQUENCE FROM N.A. STRAIN-C3H/IO1, 129/SVJ, AND 129/SVEVTAC; Reiter J.L., Threadgill D.W., Eley G.D., Strun Sinclair C.S., Pearsall R.S., Green P.J., Yee Balasubramaniam S., Crossley T.O., Magnuson T.
                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Lagomorpha; Leporid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-OCT-2001 (TrEMBLrel. 18, Last annotation
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Tetens F., Fischer B.;
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                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                              ıs (Mouse).
Metazoa; Chordata; C
→ + heria; Rodentia; {
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149
149 AA;
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149
16240 MW;
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16, Last sequence 21, Last annothing receptor isof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 723; DB 6; Let Score 723; DB 6; Let Score 723; DB 6; Let Score 720;
                                                                                                                                               Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                 t sequence upor t annotation of isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leporidae;
                                                                                                                                                                                                                                                                                                                                    643
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    Strunk K.
Yee D.,
Ison T.R.,
                                                                                                                                                                                                                                                                                                                                      ⋛
                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                                     update)
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      Lampland
James C.I
                     .E., Danielsen
Lampland A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels .,
                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuechenhoff A.,
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                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Best Local S
Matches 141
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O9WVF5;
O1-NOV-1999 (TrEMBLrel. 1
O1-NOV-1999 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
Epidermal growth factor r
                                                                                                          STRAIN-C57BL/6J; TISSUE-LIVER; Reiter J.L., Threadgill D.W., Danielsen A.J., Sche Lampland A.L., Balasubramaniam S., Crossley T.O., Maihle N.J.;
                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
    SEQUENCE FROM N.A
                                          Carboxy-Terminal Tru
Submitted (JAN-1999)
                                                                                      "Alternative
                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                            EGFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01030; Recep_L_domain; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 46.0 nes 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMYNNCEVVLGNLEITYVQRNYDLSFL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARGAA - - STOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKH 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL----QSHPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHG
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                                                                               Transcripts from the Human and Mouse
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                              Truncated Receptors.";
999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                         12, Created)
12, Last sequence update)
21, Last annotation update)
receptor (Epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 717.5; 1
Pred. No. 3.8e
39; Mismatches
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                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEF22002C84911B1 CRC64;
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                                                                                      EGFR Genes Encode
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                                                                                                                                                                                                                                                         Euteleostomi;
; Murinae; Mus
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Qkido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF124513; AAD44149.1;
EMBL; AF275366; AAG28047.1; J
EMBL; AF275364; AAG28047.1; J
EMBL; AF275365; AAG28047.1; J
EMBL; AK004944; BAB23688.1;
EMBL; AK004944; BAB236841.1;
EMBL; AK004811; BAB23662.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C3H/101, 129/SVJ, AND 129/SVETTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Daniels
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6J; 1
MEDLINE-21085660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00757; Pfam; PF01030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000494; EGFR_L_domain
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoforms
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                                   269
                                                                    186
                                                                                                    210
                                                                                                                                     130
                                                                                                                                                                   154
                                                                                                                                                                                                    08
                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                    36 ARGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFL
                                                                                                                                                                                                                                                                   20
                                                                                                                                                      GGLRELQLRSLTEILKGGYLIQRNPQLCYQDTILWKDI----FHKNNQLALTLIDTNRSR
                                                                                                                                                                                                 MGI:95294; Egfr.
SDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHG
                                  SDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACFYNYLSTDVG
                                                                  SCPKCDPSCPNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAGCTGPRE
                                                                                 ACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKH
                                                                                                                                 TGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL----
                                                                                                                                                                                                                                                                 AAGGALEEKKYCQGTSNRLTQLGTFEDHFLSLQRMYNNCEVVLGNLEITYVQRNYDLSFL
                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  655 AA;
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Recep_L_domain;
; FU; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Furin-like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER; pubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mic sequence analysis and 
Egfr transcripts encoding
                                                                                                                                                                                                                                                                                                                                                                                                   72906 MW;
                                                                                                                                                                                                                                                                                                                                                19.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of a full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
                                                                                                                                                                                                                                                                                                                                 Score 717.5; |
Pred. No. 3.9e
39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                   6B34063B1BC928CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding
                                                                                                                                                                                                                                                                                                                                                     .9e-45
                                                                                                                                                                                                                                                                                                                                                                   DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              truncated receptor
                                                                                                                                                                                                                                                                                                                                    100;
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                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collection.";
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                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                   -QSHPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K. -F.,
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                 Query Match
Best Local S
Matches 141
                                                                                                                                             Prodom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 5.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; TyrKC; 1.

SMART; SM00219; CYTOCHROME_C; UNKNOWN_1.

PROSITE; PS001190; CYTOCHROME_C; UNKNOWN_1.

PROSITE; PS001197; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.

PROSITE; PS001019; PROTEIN_KINASE_TYR; 1.

ATP-binding; Receptor; Transferase.

SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reiter J.L., Thicas
Schehl C., Pearsall R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9EP98;
Q1-MAR-2001 (TrEMBLrel. 16, Last;
Q1-MAR-2001 (TrEMBLrel. 16, Last;
Q1-JUN-2002 (TrEMBLrel. 21, Last
Epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain;
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Comparative genomic sequence analysis and isolation of human mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mGI:95294; Egfr.
erPro; IPR000345; CerPro; IPR000494; I
ARGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                v – v
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AF275364; AAG28045.1;
AF275365; AAG28045.1;
AF275367; AAG24386.1;
                                                                 141;
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                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IPR002174;
; IPR002290;
; IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000719;
                                                                 19.2%;
llarity 46.8%;
Conservative 3
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ative Egfr transc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Threadgill D.W., Eley G.D., Strunk K.E., I earsall R.S., Green P.J., Yee D., Lampland lam S., Crossley T.O., Magnuson T.R., James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                          Furin-like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Furin-like.
Ser_thr_pkinase
Tyr_pkinase.
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Euk_pkinase.
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                                                    Score 717.5; Ub ...
Pred. No. 8.7e-45;
                                                                 39;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update) annotation updat isoform 1.
                                                                                                                                                 62CD021C9DE32E18
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                                                                                                                                                   CRC64;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       James
                                                                                                        Length
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danielsen
d A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
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                                                                                                          1210;
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                                                                 Gaps
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RESULT
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Pfam; PF00069; pkinase; 1.

Pfam; PF01030; Recep_L_domain; 2.

Pfam; PF01030; Recep_L_domain; 2.

PRINTS; PR00109; TYRKINASE;

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TYFKC; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

ATP-binding; Receptor; Transferase; Tyrosi
SEQUENCE 1209 AA; 134891 MW; 96FEE7F6C
                                                                                                                                                                                          EMBL;
                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Epidermal growth factor
                                                                                                                                                                                                                 Guttridge K., Dawson T.I
Submitted (NOV-1999) to
                                                                                                                                                                                                                                                                                                                                   "A truncated, secreted form of the epidermal growth factor encoded by an alternatively spliced transcript in normal mol. Cell. Biol. 10:2973-2982(1990).
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-FISHER; TISSUE-LIVER; MEDLINE-90258888; PubMed-2342466; Petch L.A., Harris J., Raymond V.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                        InterPro;
                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                 STRAIN-FISHER;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVG
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                                                                                                                   Pro; IPR001245; Tyr_pl
PF00757; Furin-like;
PF00069; pkinase; 1.
                                                                                                                                                                                          M37394; AAF14008.1;
P11362; 1FGK.
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                                                                                                                                                       ; IPR000719; ; IPR002174;
                                                                                                                                                                                                                                                                           (NOV-1991)
                                                                                                                                                                                IPR000494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                         TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                   TISSUE-LIVER;
                                                                                                                                                                                                                  T.L., E
                                                                                                                                                                                                                                                                           ç
                                                                                                                                                        Euk_pkinase.
Furin-like.
                                                                                                                                                                                EGFR_L_domain.
                                                                                                                                            Tyr_pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13, Created)13, Last sequence update)21, Last annotation updat receptor.
                                                                                                                                                                                                                 Earp H.S.;
• EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
  e; Tyrosine-protein kinase.
96FEE7F6CC1B7773 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                    Lee
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                                                                                                                             Query Match
Best Local S
Matches 180
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Best Local
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUE-GASTRO-DUODENAL MUCOUS;

TACCHIEF J.A., Majumdar A.P.N.;
                                                                                                                                                                         Receptor.
SEQUENCE
                                                                                                                                                                                                               regulator of EGFR.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF189818; AAG17037.2;
Interpro; IPR000494; EGFR_L_domain.
Interpro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                           01-MAR 2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor related protein.
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ESE0
                                                                                                                                                                                                                                                                     Yu Y., Moshier J.A., Majumdar A.I
"Cloning of a novel EGFR-related
                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ESEO;
                                                                                                                                                                                            Pfam; PF01030; Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
   130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303
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                       154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 142; Conserv
KTIQEVAGYFLIALNTVERIPSEDLQIIRGNALYENTYALAILSN
                                                     S-RACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGG?A-RCKGPLPTDCCHEQCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVGS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLTGCPKCDPSCPNGSCWGRGEENCQKLTKIICAQQCSRRCRGRSPSDCCHNQCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLAALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRESDCLVCHRFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -YGTNKTGLRELPMRNLQEILIGAVRFSNNPILCNMETIQWRDIV-QDVFLSNMSMDVQR
                                                                                                                               180;
                                                                                                                                       Similarity
                                                                                                                                                                         478
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                         A
                                                                                                                                                                                                         Furin-like;
                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                         53233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.18;
                                                                                                                            18.8%; Score 704.5; DB 11 34.5%; Pred. No. 2.4e-44; ive 62; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 714.5; DB 11;
Pred. No. 1.5e-44;
42; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                        CF873A8376Ç519E5 CRC64;
                                                                                                                                                                                                                                                                     peptide: A putative negative
                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                DB 11; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1209
                                                                                                                           , 66
                                           --YGTNR
                                                                                                                                                                                                                                                                                                                                      Rattus
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                                                                                                                            Gaps
                                                                                    79
                                                                                                       93
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                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 139; Conserv
                                                                                                                                                                                                                                                                                        EMBL; BC002706; AAH02706.1; -...
Interpro; IPR000494; EGFR_L_domain.
Interpro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00130; Recep_L_domain; 1.
SMART; SM00261; FU; 2.
SEQUENCE 331 AA; 36489 MW; 45B8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                  nomolog 3.
Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to v-erb-b2 avian erythroblastic leukemia v
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9вир7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9вир7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
                                                                             117
                                                                                           133 LAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306
 252
                                                   193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347
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                                                                                                                               57
                                                                                                                                                         73
                                                                                                                                                                                   10
                                                                                                                                                                                                            16
                                                                                                                                                                                                   LGFLFLLFFWLDRSVLAKELARGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFG
                                            HKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLP
                                                                                                                                            LGLLF-----SLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFVM-----LNYNT----NSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIV
                                                                                                                              EVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAVVGLNITSLPWQVPSLSWQAVTRPLHPLAQNRVSWDTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AAPQPHPPPAFS-----PAFDNLYYWDQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPAARPAGATLERAKTLSPGKNGVV------KDVFAFGGAVENPEYL---TPQGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTLSI---NATNIKHFKYCTAI----SGDLHILPVA----FKGDSFTRTPPLDPRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLOSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAK
                           RDRD---AEIVVKDNGRSCPPCHEVCKG-RCWGPGSEDCQTLTKTICAPQCNGHCFGPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCPKCDPSCPNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAGCTGPQK
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LEILKTVKEITGSLLIQAWPENWTDLHAF----ENLEIIRGRTKOHGOFS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCVRACGPD----YYEVEEDGIRK-CKKCDGPCRKVCNG-IGIGEFK
                                                                                                                                                                                                                                                                                         36489 MW; 45B8EBEE683FE7E8 CRC64;
                                                                                                                                                                                                                                                18.6%;
                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                     Score 697; DB 4;
Pred. No. 5.3e-44;
15; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519
                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328
  311
                                                   251
                                                                             167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 6,
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01030; Recep_L_domain; 2.
PRINTS; PR00109; TYRKINASE.
ProDom; DD000001; Euk_pkinase; 1.
SMART; SM00261; EU; 3.
SMART; SM00219; Tyrkc; 1.
PR0SITE: PS00190; CYTCCHROME_C; UNKNOWN_1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00107; PROTEIN_KINASE_DOM; 2.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98241172; PubMed-9582016; Dimitrijevic N., Winkler C., Wellbrock C., Altschmied J., Schartl M.; Wellbrock G., Activation of the Xmrk proto-oncogene of poverexpression and mutational alterations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9YH40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XMRK.
Xiphophorus xiphidium.
Xiphophorus xiphidium.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin like.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2000) to the EMBL; U53471; AAD10500.2; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-RIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-RIO PURIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
     163
                                                                                                    103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
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                                                    85
                                                                                                                                                   28
                                                                                                                                                                                                43
                                                                           VLTAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR
                                                                                                                                                                     QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGY 102
SLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSR
                                                                                                                                            KVCQGTSNQMTM---LDNHYLKMKKMYSGCNVVLENLEITYTQENQDLSELQSIQEVGGY
                                             GVCVASCPHNFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNPHTKYQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF01030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASCVTACPYNYL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00757; Furin-like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16:1681-1690(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000345; CytC_heme_bind
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
rosine kinase proto-oncogene.
                                                                                                                                                                                                                                                Conservative
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6; Mismatches
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Pred. No. 7.
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7F7EE38D8771A74E CRC64;
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Best Local Similarity
Matches 121; Conserv
                                                                                                                                                                       HSSP; P04141; 2GMF.
Interpro; IPR000773; GM_CSF.
Pfam; PP01109; GM_CSF; 1.
PRINTS; PR00693; GM_CSFACTOR.
PrODOM; PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
PROSITE; PS00702; GM_CSF; 1.
VARIANT 60 60 V
                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Granulocyte-macrophage colony-stimulating factor.
GM-CSF.
                                                                                                                                                                                                                                              naturally infected with Ebola (Reston).";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AY007376; AAG16626.1; -.
HSSP; P04141; 2GME.
                                                                                                                                                                                                                                                                                         Hutchinson K.L., Villinger F., Mi Peters C.J., Rollin P.E.; "Multiplex analysis of cytokines
                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; V.
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecina; Macaca.
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                   DCWEPVQE
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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EGFR_MOUSE
EGFR_HUMAN
CSF2_HUMAN
CSF2_SHEEP
EGFR_DROME
CSF2_CGEFL
CSF2_PIG
CSF2_CAVPA
CSF2_FELCA
CSF2_FELCA
CSF2_ROUSE
CSF2_MOUSE
ILPR_BRALA
ERB2_MOUSE
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ERB2_MOUSE
ILRR_BOME
INSR_HUMAN
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P04141 homo sapien Q62799 rattus norv P13388 xiphophorus P28773 ovis aries P04412 drosophila P51748 cervus elap Q29118 sus scrofa P11052 bos taurus P48749 canis famil O62757 felis silve P48750 rattus norv Q60481 cavia porce P24348 caenorhabdi P01587 mus musculu O02466 branchiosto P70424 mus musculu O25197 hydra atten P09208 drosophila P06213 homo sapien P15208 mus musculu Q25410 lymnaea sta O9wtl4 mus musculu P15127 rattus norv P14616 homo sapien
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P13387 gallus gall
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ID ERB2_H
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DT 13-AUG
DT 15-JUN
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GN ERBB2
OC EUKARY
OC Mammal
OX NCBLT
RN [1]
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(C P04626;
(C P04626)
(T 13-AUG-1987 (Rel. 05, Created)
(T 13-AUG-1987 (Rel. 05, Last sequence update)
(T 13-AUG-1987 (Rel. 05, Last sequence update)
(T 13-AUG-1987 (Rel. 05, Last sequence update)
(T 15-JUN-2002 (Rel. 41, Last annotation update)
(T 15-JUN-2002 (Rel. 41, Last annotation update)
(T 16-JUN-2002 (Rel. 41, Last annotation update)
(T 18-JUN-2002 (Rel. 05, Last sequence update)
(T 18-JUN-2002 (Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355
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157.5	160	162	166	168	178	207	228.5	233.5	235.5	246	246.5
4.2	4.3	4.3	4.4	4.5	4.8	5.5	6.1	6.2	6.3	6.6	6.6
605	830	1321	707	386	2715	1390	581	1373	1370	1367	1300
_	<u></u> -	-	_	۲	1	_	_	۲	_	ᆫ	_
BRL1_EBV	SREC_HUMAN	IRS2_MOUSE	SFPQ_HUMAN	PPAP_HUMAN	TRX2_HUMAN	INSR_AEDAE	IRR_RAT	IG1R_MOUSE	IG1R_RAT	IG1R_HUMAN	IRR_CAVPO
P03209	Q14162	P81122	P23246	P15309	Q9umn6	Q93105	Q64716	Q60751	P24062	PC8063	P14617
epstein-bar	homo sapien	mus musculu	homo sapien	homo sapien	homo sapien	aedes aegyp	rattus norv	mus musculu	rattus norv	homo sapien	cavia porce

ALIGNMENTS

2.7.1.112) kinase-type

cell .

	-!- SUBCELLULAR LOCATION: Type I membrane protein.	88
	(POTENTIAL)	C
	tyrosine phosphate. -i- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS	88
	-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein	8
•		င္ပ
:	POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-	റ്റ
		දු
	-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,	റ്റ
	Genomics 15:426-429(1993).	RL
	specific competition hybridization.";	RT
	"Characterization of a new allele of the human ERBB2 gene by allele-	RT
	Ehsani A., Low J., Wallace R.B., Wu A.M.;	RA
	MEDLINE=93194196; PubMed=8095488;	RX
	VARIANTS VAL-654 AND VAL-655.	RP
		RN
	Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).	R.
	human salivary gland adenocarcinoma.";	RΤ
	c-erbB-1/epidermal growth factor-receptor gene and is amplified in a	RΤ
	"A v-erbB-related protooncogene, c-erbB-2, is distinct from the	RT
	Semba K., Kamata N., Toyoshima K., Yamamoto T.;	RA
	MEDLINE=86016729; PubMed=2995967;	RX
	SEQUENCE OF 737-1031 FROM N.A.	RΡ
	[3]	RN
	Science 230:1132-1139(1985).	RL
	shares chromosomal location with neu oncogene.";	RΤ
	"Tyrosine kinase receptor with extensive homology to EGF receptor	RΤ
	Francke U., Levinson A., Ullrich A.;	RA
	McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J.,	RA
	Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A.,	RA
	MEDLINE=86070181; PubMed=2999974;	RX
	SEQUENCE FROM N.A.	RP
	. [2]	RN
	Nature 319:230-234(1986).	RL
		ΡŢ
	"Similarity of protein encoded by the human c-erb-B-2 gene to	RТ
	Saito T., Toyoshima K.;	RA
	Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,	RA
	MEDLINE-86118663; PubMed-3003577;	RX
	SEQUENCE FROM N.A.	RP

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PARAMETER PRODECTION OF A CONTRACT OF A CONT
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Pfam; PF010757; Fur:
Pfam; PF01030; Recc
Pfam; PF02757; YLP
Pr0D0m; PD000001; I
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SMART; SM00219; TyrKC; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
    DOMAIN
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NP_BIND
BINDING
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism.
SIGNAL
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SMART; SM00219; TyrKc
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. M1776; AAA35808.1; ...
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. M1790; AAA35978.1; ...
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RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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IPR002174; Furin-like.
IPR001245; Tyr_pkinase.
IPR004019; YLP_motif.
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Furin-like; 1.
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lng; Phosphorylation;
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       KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY
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                                                                                                FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI
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MEDLINE-92155181; Gullick W.J., Botto
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P06494;
01-JAN-19
                                                                     "An extended family of protexpressed in the vertebrate Neuron 6:691-704(1991).
                                                                                                                                                                               Nature
[2]
                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                          receptor-related ERBB2 OR NEU.
                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
15-DEC protein-tyrosine kinase erbB-2 precursor (EC 2)
(p185erbB2) (NEU prote-oncogene) (C-erbB-2) (Epidermal
                                                                                                                                                                                                                   Bargmann C.I., Hung M.-C., We
"The neu oncogene encodes an
protein ":
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TISSUE-Neuroblastoma;
MEDLINE-86118662; PubMed-3945311;
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                                                                                                                                                  SEQUENCE OF 852-905 FROM TISSUE-Sciatic nerve;
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181; PubMed=1346763;
Bottomley A.C., Lof
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prate nervous system.";
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Sciurognathi; Muridae;
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PROSITE; PS00109; PROTEIN_
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Pfam; PF02757; YLP; 2.
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SUBUNIT:
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ogenic and oncogenic forms of the new protein.";

O J. 11:43-48[1992],

FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,

ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A

POTENTIAL LICAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-

ALPHA AND AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial
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IPR000719;
               e; Glycoprotein; Multigene family; Receptor; Signal; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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a collabora	RESIDUES. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY. SWISS-PROT entry is copyright. It is produced thro	11	8888
SINE	TYPE I Membrane protein. SUBCELLULAR LOCATION: Type I membrane protein. PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROS	: :	888
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protein	AMPHIREGULIN (BY SIMILARITY). ACTIVITY: ATP + a protein tyrosine = ADP +	-	88
SP30 IS	ALTHOUGHT REGREGATION OF THIS RECEPTOR. NOT ACTIVATED BY EGF,	-	888
COMPLE	CIONING AND ACCEVATAL OF A NEIRECHITA RECEDIDADA - I - FINCTION: ESSENTIAL COMPONENT OF A NEIRECHITA RECEDITOR	Gene	3 2 2
)	jima T., IShizaka Y., Nagao M., Arai M.	Naka Yama	RR
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	(_TaxID=10036;	NCBI	RQ
5	a; Rodentia; Sclurognathi; Muridae;	Mamm	888
in n	a: Chordata: Craniata: Vertebrata: Eute	Meso	888
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RESULT 4

EGFR_CHICK
ID EGFR.C

AC P13387
DT 01-JAN
DT 15-JUN
CG GALLUS
OC GALLUS
OC GALLUS
OC RT CANAI
RA ULLTA
RA WEDLIT
RA WEDLIT
RA ULLTA
RA "Chick
RT "CC -1- E
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                                                                                                                                                                                                                  EMBL; M20386; AAA48760.1;
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR0021745; Tyr_pkinase.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
SMART; SM00261; FU; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAX I., Johnson A., Howk R., Sap J., Bellot F., Winkler M., Ullrich A., Vennstrom B., Schlessinger J., Givol D., "Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mouse cells, and differential binding of EGF and transforming growth factor alpha.";
Mol. Cell. Biol. 8:1970-1978 (1988).

-I- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL O AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, G VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine bhosphate
                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Cr
01-JAN-1990 (Rel. 13, La
15-JUN-2002 (Rel. 41, La
Epidermal growth factor
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                                                                                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SUBCELLALIAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of e
synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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                                                                          PS00107; PROTEIN_KINASE_ATP; F
PS00109; PROTEIN_KINASE_TYR; F
PS0011; PROTEIN_KINASE_DOM; F
brane; Glycoprotein; Receptor;
r-protein kinase; ATP-binding; F
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Last sequence update)
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or receptor precursor (E
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r; Signal; Transferase;
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                                                                            Phosphorylation.
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GP30 At
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Best Local :
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                                    SEGAGSDVFDGDLGMGAAKGLQSL 393
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                                                                                  FGATCVRECPHNYVVTDHGSCV-----
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77427
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BY SIMILARITY.
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Pred. No. 1.
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GILCNAC.
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RESULT 5
EGFR_HUMAN
ID EGFR_HUMAN

STANDARD;

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Reiter J.L., Inc., Schehl Sinclair C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PO0533; PO6268; Q14225; Q9UMD7; Q9UMD8; Q9UMG C00688; Q9BXS2; Q9HZC9; Q9EXX1, Q9H3C9; Q1-VLL-1986 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epidermal growth factor receptor precursor (b protein-tyrosine kinase ErbB-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Possible role of variant RNA transcripts in epidermal growth factor receptor expression i Mol. Reprod. Dev. 41:149-156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W., Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J., Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.; "Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells."; Nature 309:418-425(1984).
                                                                                                      "Human and mouse alternative EGFR transcripts extracellular domain of the receptor."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
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Mammalia; Eutheria; Primates;
          "Expression cloning of human EGI
amplification and three related
                                     Lin C.R., Ch
Evans R.M.,
                                                                 MEDLINE-84196372;
                                                                                                                                                 Maihle N.J.;
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                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                  mouse
                                                                                                                                                                                                                                                               "Comparative
                                                                                                                                                                                                                                                                             Maihle N
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                                                                                                                                                                                                                                                                                                                                                    TISSUE-Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97256547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A 1.8 kb alternative transcript from the factor receptor gene encodes a truncated Nucleic Acids Res. 24:4050-4056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97078686;
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MEDLINE-84219729; PubMed-6328312;
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                                                                                                                                                                                                                                                  alternative
OF 713-924 FROM N.A.
4196372; PubMed-6326261;
Chen W.S., Kruiger W., Stolarsky L.S., Weber W.,
Verma I.M., Gill G.N., Rosenfeld M.G.;
4., Verma I.M., Gill G.N., Rosenfeld M.G.;
ion cloning of human EGF receptor complementary DNA:
                                                                                                                                                                                             ဝ္ရ
                                                                                                                                                                                                                      71:1-20(2001).
                                                                                                                                                               575-687 FROM N.A., Threadgill D.W., L., Balasubramaniam
                                                                                                                                                                                                                                                                                      Threadgill D.W., Eley G.D., Strunk K.E., Danielsen air C., Pearsall R.S., Green P.J., Yee D., Lampland iam S., Crossley T.D., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                genomic sequence analysis ative EGFR transcripts enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maihle
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                                                                                                                                                               Danielsen A.J
m S., Crossley
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                                                                                                                                                                                                                                                encoding truncated receptor
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growth factor receptor-like
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Smith K.D., Davies M.J., Bailey D., Renouf D.V. "Analysis of the glycosylation patterns of the the epidermal growth factor receptor expressed ovary fibroblasts.";
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"Human epidermal growth factor receptor variety of RNAs overproduced in A431 car Nature 309:806-810(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84245835; PubMed-6330563; Xu Y.H., Ishii S., Clark A.J.L., Roe B.A., Merlino G.T., Pastan I.
                                                                                                                                      Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M. Howk R., Givol D., Ullrich A., Schlessinger J.;
"All autophosphorylation sites of epidermal growth factor (EG receptor and HER2/neu are located in their carboxyl-terminal Identification of a novel site in EGF receptor.";
J. Biol. Chem. 264:10667-10671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Contributory effects of de novo transcription and transcript termination in the regulation of human factor receptor proto-oncogene RNA synthesis."; Blol. Chem. 266:1746-1753(1991).
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                                                                                                                                                                                                                                       "ATP-stimulated interaction and supercoiled DNA."; Nature 309:270-273(1984).
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[8]
                   CARBOHYDRATE-LINKAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. 127:65-72(2000)
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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TISSUE SPECIFICITY: Expressed in
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ON: Receptor for EGF, but a
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15-UNN-2002 (Rel. 41, Last annotation update)
Receptor protein tyrosine kinase erbB-4 precursor (EC (p180erbB4) (Tyrosine kinase-type cell enveron (EC
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Mammalia; Eutheria;
                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phorbol ester."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klagsbrun M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fetal brain; MEDLINE-97476287; PubMed-9334263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS JM-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lenius K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                  - SUBCELLULAR LOCATION: Type I membrane protein
- ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER
FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESS
BUT NOT JM-B. SO. THEY RESPECTIVELY REPRESENT CLEAVABLE AND
NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED
CERREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,
KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARACHYROID, CEREBELLUM,
PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS,
LUNG, SALIVARY GLAND, AND PANCREAS.
                                       Ween the Swiss institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                     tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH
                                                                                                                                                                                                                                                                                                                                                                                                  NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN CATALYTIC ACTIVITY: ATP + a protein tyrosine -
                                                                                                                              SIMILARITY: BELONGS TO THE
                                                                                                                                                          PTM: LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                    RECEPTORS (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                NTAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: SPECIFICALLY BINDS
                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSL
                                                                                                                                                                                                                                                                                                                                                                                                                               11. Chem. 272:26761-26768(1997).
INCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY INCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY INCTION: SPECIFICALLY BINDING EGF-LIKE GROWTH FACTOR, NRG-3, HEBARIN-BINDING EGF-LIKE GROWTH FACTOR, INDUCES CELLAK, INTERACTION WITH THESE FACTORS INDUCES CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 juxtamembrane domain isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differential
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                                                                                                                              EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi C.J., Rio C., Plowman
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                                                                                                                              RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of HER4/ErbB4. Isoform-specific processing in response to
                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine -
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                                                                               a collaboration -
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; FurIn-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
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PROSITE; PS00109;
PROSITE; PS50011;
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SMART; SM00261; F
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P11362; 1FGK.
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SM00219; TyrKc;
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PROTEIN_KINASE_DOM;
                                               Euk_pkinase;
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N-LINKED (GLCNAC...) (E
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RECEPTOR PROTE
EXTRACELLULAR
POTENTIAL.
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n kinase; A
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ATP-binding; Phosphorylation;
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Query Match
Best Local S
Matches 142
                                                                                                  STRAIN-BALB/C;
Hibbs M.L.;
Submitto
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                               SEQUENCE FROM N.A.
STRAIN-B6/C3; TISSUE-Liver;
MEDLINE-94170986; PubMed-8125255;
Luetteke N.C., Phillips H.K., Qiu
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EGFR_MOUSE
Q01279;
"The mouse waved-2 phenotype receptor tyrosine kinase."; Genes Dev. 8:399-413(1994).
                                                                                                                                                                                                  STRAIN-BALB/c, an MEDLINE-93126380;
                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BALB/c, and CD-1;
                                                                                                                                                                                                                                               Avivi A., Skorecki K., Yayon A., "Promoter region of the murine f. (bek/KGFR) gene.", Oncogene 7:1957-1962(1992).
                                                                                                                                                                                                                                                                                             STRAIN-BALB/C; TI
MEDLINE-93026370;
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
Mammalia;
                                                                                                                                                       Paria B.C., Das S.K., Andrews "Expression of the epidermal in mouse blastocysts during d Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
NCBI_TaxID=10090;
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LB/c; TISSUE=Liver;

3026370; PubMed=1408137;

Skorecki K. Yayon A.
                                                                                                   (APR-1994)
                                                                                                                                                                                                                                                                                                                                          is (Mouse).
Metazoa; Chordata; C
martheria; Rodentia; S
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                                                                                                                                                                                    380; PubMed=7678348;
s S.K., Andrews 7
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                                                                                                                        N.A.
TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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. 33, Last sequence update)
. 41, Last annotation update)
factor receptor precursor (E
                                                                                                                                                         , Andrews G.K., Dey S.K.;
pidermal growth factor receptor
during delayed implantation.";
i. U.S.A. 90:55-59(1993).
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Pred. No. 2.6e
12; Mismatches
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Pfam; PF00069; pkinase; 1.

Pfam; PF01030; Recep_L_domain; 2.

Pfam; PF01030; Recep_L_domain; 2.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X78987; CAA55587.1; -.
EMBL; U03425; CAA42219.1; -.
EMBL; L06864; AAA53029.1; -.
EMBL; L106864; AAA53029.1; -.
EMBL; L12608; CAA78249.1; -.
HSSP; P11362; 1FGK.
MGD; MGI:95294; EGFR_L_dc
InterPro; IPR000494; EGFR_L_dc
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SEQUENCE OF 1
TISSUE-Brain;
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Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SI
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a control between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatical the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91232866; PubMed=2030916;
Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.;
"Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                Tyrosine-prote
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SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex. Induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            i:95294; Egfr. L_domain.
j; IPR0001494; EGFR_L_domain.
j; IPR000119; Euk_pkinase.
j; IPR002174; Furin-like.
j; IPR001245; Tyr_pkinase.
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Pred. No. 3.7e-32;
9; Mismatches 100;
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the Euro
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J. Neurosci. 17:1642-1659(1997).
-I- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTERACTION HITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY).
-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1031-1198 FROM N.A.
STRAIN-Sprague-Dawley: TISSUE-Spinal cord;
MEDLINE-97184211; PubMed-9030624;
                                       Pfam;
Pfam;
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HSSP;
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J. Biol. Chem. 273:10261-10269(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao Y.-Y., Sawyer D.R., Baliga
Marchionni M.A., Kelly R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                             PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extended family of protein-tyrosine kinase genes differentially ressed in the vertebrate nervous system."; ron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                                                                                                              RECEPPORS (POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING
TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING
NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
HEART.
                                                                                                                                                                                                                                                                                         3 SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN 
European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                   rrPro; IPR000494; EGFF

rrPro; IPR000719; Euk,

rrPro; IPR0002174; Furi

rrPro; IPR001245; Tyr,

rrPro; IPR004019; YLEP,

rrPro; Furin-1ikc,

rrP00069; pkinase; J
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SUBUNIT: HOMODIMER OR HETERODIMER
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U52531; AAC53051.1;
P11362; 1FGK.
; PD000001; SM00261;
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                                                                     57; Furin-like;
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                                         Recep_L_domain;
YLP; 2.
                                                                                                                                                                                                    AAD08899.1;
                           TYRKINASE
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Baliga R.R.,
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          Euk_pkinase;
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Tyr_pkinase.
YLP_motif.
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tors, ErbB2 and
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RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                       "C-erbB3 gene encodes secreted a tyrosine kinase.";
Biochem Biophys. Res. Commun. 1
-!- FUNCTION: BINDS AND IS ACTIV-
-!- CATALYTIC ACTIVITY: ATP + a
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"Isolation and characterization of ERBB3, a third member
ERBB/epidermal growth factor receptor family: evidence fo
overexpression in a subset of human mammary tumors.";
Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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Katoh M., Yazaki Y.,
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Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990).
[3]
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15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(C-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
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                                                                                              SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SIZ OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE (BY SIMILARITY).
DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM
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SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
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Y., Sugimura T., Codes secreted as v
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tney G.S., Neubauer
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InterPro; IPR000719; I
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SMART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG
PROSITE; PS00109; PROTEIN_KINASE_TYR; FALSE_NEG
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene family; 1
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                                                                        cantrell M.A., Anderson D., Cerretti D.P., Pri
Tushinski R.J., Mochizuki D.Y., Larsen A., Gra
"Cloning, sequence, and expression of a human
colony-stimulating factor.";
Proc. Natl. Acad. Sci. U.S.A. 82:6250-6254(198
                                                                                                                                                                                                                                                                                                                                                                                                                                   cells
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MEDLINE-85242684; PubMed-3925454;
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Mammalia; Eutheria;
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SEQUENCE FROM N.A MEDLINE-85218749; Wong G.G., Witek
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MEDLINE=85298329; PubMed=3898082;
                                                                                                                                                                                                                                                 "Genomic cloning, activity of human Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-86205844; Publ
Kaushansky K., O'Hara
                                                                                                                                                                                                                                                                                                                                                                                                                                                    colony-stimulating factor
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Arai K.-I., Rennick
"Isolation of cDNA f
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15-JUN-2002
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                                                                                                                                                                                                                                               characterization, and multilineage growth granulocyte-macrophage colony-stimulating Sci. U.S.A. 83:3101-3105(1986).
  PubMed=3923623;
J.S., Temple P.A.,
                                                                                                                                                                                                                                                                                                                             PubMed=3486413;
Hara P.J., Berkner
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for a human granulocyte-macrophage
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Pred. No. 5.4e
15; Mismatches
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Catarrhini; Hominidae;
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Grabstein
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K., Cosman
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Davis C.A., Kadner K., Miguel Subramanian S., Martin C.H.; Submitted (MAR-1998) to the EM [7]
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"Novel fold and putative receptor binding
granulocyte-macrophage colony-stimulating
Science 254:1779-1782(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human granulocyte macrophage colony-stimulating factor in genetical engineered and normal mesenchymal cells.";
Biochemistry 31:1881-1886(1992).
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Kimmerly
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                                                                                                                            This
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J. Mol. Biol. 224:1075-1085(1992)
-!- FUNCTION; CYTOKINE THAT STIMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86030234; PubMed=3876930; Miyatake S., Otsuka T., Yokota T., "Tructure of the chromosomal gene stimulating factor: comparison of EMBO J. 4:2561-2568(1985).
                                                                                                                                                                                                                                                                                                                                                                    Walter M.R.,
Bugg C.E.;
                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-92235844; PubMed-1569568;
Walter M.R., Cook W.J., Ealick S.E., N
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Science 228:8
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"Human GM-CSF:
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Kaushansky K., Loj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                        "Three-dimensional structure of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                            PHARMACEUTICAL: Available under the names Leukine (Immunex) at Leucomax (Novartis). Used in myeloid reconstitution following marrow transplant, bone marrow transplant engraftment fallure delay, mobilization and following transplantation of autologo peripheral blood progenitor cells, and following induction chemotherapy in older adults with acute myelogenous leukemia. DATABASE: NAME-Leukine; NOTE-Clinical information on Leukine;
                                                                                                                                             DATABASE: NAME-Leukine; NOTE-Clinical information www-"http://www.imunex.com/patient/pa02e1.html"
                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                  POLYMORPHISM:
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                                                                                                                                                                                                                                                                                           GRANULOCYTES, MACROPHAGES,
                                                                                                                                                                                                                                                                                                      OF HEMATOPOIETIC PRECURSOR
                                                                                                              SWISS-PROT entry is copyright. It is produced through a casen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ansky K., Lopez J.A., Brown C.B.; of carbohydrate modification in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GM-CSF: molecular cloning ation of the natural and 228:810-815(1985).
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Pitluck S
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                                                                                                                                                                                                                                                                                                                                                                                  Nagabhushan
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Hewick R.M.,
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S., Pollard M.,
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CARBOHYD
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CARBOHYD
              ERB3_RAT STANDARD; PRT; 1339 AA G62799; Q62995; 15-DEC-1998 (Rel. 37, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
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Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01109; GM_CSF; 1.
Pfam; PF01109; GM_CSF; 1.
PRINTS; PR00693; GMCSFACTOR.
ProDom; PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
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                                                                                                                                                                                                                                                       809
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C24636; C24636.
A25169; A25169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1CSG; 31-JAN-94.
2GMF; 08-NOV-96.
                                                                                                                                                                                 DCWEPVQE 675
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127; Conserv
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M10663; AAA52121.1;
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O-LINKED.
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ation update)
erbB-3 precursor
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   Pram; Froud, Recept_domain; 2.

{    PRINTS; PR00109; TYPKKINASE.

    PRODOM; PD000001; Euk_pkinase; 1.

    SMART; SM00261; FU; 5.

    R SMART; SM00261; FU; 5.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS0011; PROTEIN_KINASE_TYR; 1.
Transferase;
SIGNAL
CHAIN
CHAIN
TRANSMEM 6
DOMAIN 6
DOMAIN 1
DOMAIN 7
                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkin
InterPro; IPR002174; Furin-11
InterPro; IPR0021745; Tyr_pkin
Pfam; PF00059; pkinase; 1.
Pfam; PF00757; Furin-1ike; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUE-Sciatic nerve;
MEDLINE-97184212; PubMed-9030624;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
"Expression of neuregulins and their putative receptors, ErbB2 and
ErbB3, is induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997)
-i- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                 EMBL; U29339; AAC28498.2; -. EMBL; U52530; AAC53050.1; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentitles remaines a license and the statement of th
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Hellyer N.J., Koland
Submitted (DEC-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hellyer N.J., Kim H.-H., G "Cloning of the rat ErbB3 recombinant protein."; Gene 165:279-284(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-96096535; PubMed-8522190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L.,
"Cloning of the rat ErbB3 cDNA and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUN PHOSPHATIDYLINOSITOL 3-KINASE.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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663
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707
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964
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Furin-like.
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   CYTOPLASMIC (POTENTIAL).
CYS-RICH.
PROTEIN KINASE.
                                                                RECEPTOR PROTEIN-TYROSINE KINASE EXTRACELLULAR (POTENTIAL).
                                                  POTENTIAL.
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                                                                                                          Receptor; Signal; ing; Phosphorylation.
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ERBB-3

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Matches 136
                   XMRK_XIPMA STAN
P13388;
01-JAN-1990 (Rel. 1
16-OCT-2001 (Rel. 4
15-JUN-2002 (Rel. 4
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mes 136; Conservative
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      receptor
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                     13, Created)
40, Last sequence up
41, Last annotation
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Pred. No. 2.1e
44; Mismatches
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No. 2.
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      InterPro; IPRO00494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001030; Euk_pkinase; 1.
Pfam; PF001030; Recep_L_domain; 2.
PfINTS; PR00109; TYRKINASE.
PFODOm; PD000001; Euk_pkinase; 1.
SMART; SM00210; FTU; 5.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYRKC; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS001109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Receptor; S.
Transmembrane; Glycoprotein; Receptor; S.
                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00107; PROTEIN_KINASE_ATP; PROSITE: PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM; Transmembrane; Glycoprotein; Receptor; Tyrosine-protein kinase; ATP-binding; FSIGNAL 1 25
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PIR; S06142; S
HSSP; P11362;
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Submitted (JUL-2000) to the
-!- FUNCTION: PROBABLE RECEP
-!- CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-90015140; PubMed=2797166;

Wittbrodt J., Adam D., Malltschek B., Mau
Telling A., Robertson S.M., Schartl M.;

"Novel putative receptor tyrosine kinase
inducing Tu locus in Xiphophorus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xiphophorus maculatus (Southern platyfish).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Cyprimodontiformes; Poecillidae; Xiphophorus.
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SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MI
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
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2; 1FGK.
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RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
RECEPTOR WITH PROTEIN - ADP + protein
POTENTIAL:

POTENTIAL:

CYTOPLASMIC GOTENTIAL

CYTOPLASMIC GOTENTIAL:

PROTEIN KINASE

ATP (BY SIMILARITY).

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BY SIMILARITY.

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EXTRACELLULAR
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3; 1.
4; 1.
1; Signal; Transferase;
3; Phosphorylation; Proto
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                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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MBL outstation -
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Best Loc
Matches
                                                               Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Caprinae; O'
NCBI_TaxID=9940;
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P28773;
01-DEC-1992
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01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Granulocyte-macrophage colony-stimulating fac
(Colony-stimulating factor) (CSF).
SEQUENCE FROM N.A.
MEDLINE-92039044; PubMed-1937025;
MCInnes C.J., Haig M.C.K.;
"Cloning and expression of a cDNA
                                                                                                                                                                                                                                            SHEEP
                                                                                                                      Ovis aries
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Local Similarity
hes 142; Conserv
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; Cetartiodactyla; Ruminantia; Peo
Ovis.
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Best Local Sin
Matches 102;
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DISULFID
CARBOHYD
SEQUENCE
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SIGNAL
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105
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EGFR_DROME STANDARD; PRT; 1426 AA.

p04412; 061601; 09W2G0; P81868;

13-AUG-1987 (Rel. 05, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Epidermal growth factor receptor precursor (EC 2.7)

(Gurken receptor) (Torpedo protein) (Drosophila re.

EGFR OR TOP OR C-ERBB OR DER OR CG10079.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancri
Insecta; Pterygota; Neoptera; Endopterygota; Dipte;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila

NCB_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulocyte-macrophage colony-stimulating factor.";
Gene 105:275-279(1991).
-1- FUNCTION: CYTOKINE THAT STIMULATES THE GROWTH AND DIFFERENTIATION
OF HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING
ORNAULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES (BY
                                                                SEQUENCE FROM N.A. (ISOFORMS TYPES MEDLINE=94350209; PubMed=8070664; Clifford R., Schupbach T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.ish-sib.or send an email to license@isb-sib.ch).
Clifford R., Schupbach T.;
"Molecular analysis of the Drosophila EGI
that several genetically defined classes
subdomains of the receptor protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00693; GMCSFACTOR. ProDom; PD007349; GM_CSF; 1. SMART; SM00040; CSF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P04141; 2GMF.
InterPro; IPR000773; GI
Pfam; PF01109; GM_CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outs! European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for contified and this statement is not removed.
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SUBUNIT: MONOMER (BY SIMILARITY)
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138
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79.78;
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GRANULOCYTE-MACROPHAGE
FACTOR.
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N-LINKED (GLCNAC...
W; ABAAC8733B580008 (
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Pred. No. 6.4e-24;
1; Mismatches 15;
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                                                                                                                                                                      ata; Pancrustacea;
ota; Diptera; Brac
Drosophila.
                        of
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a relative (
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AND MUTATION

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Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Buntaides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Buller H., Cadleu E., Center A., Chandra I.,
RA Gerbies B., Detcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gerbies B., Detcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Lillam A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lin X.,
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Clifford P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99102120; PubMed=9882502;
Lesokhin A.M., Yu S.-Y., Katz J., Baker N.
"Several levels of EGF receptor signaling
specification in wild-type, Ellipse, and n
Dev. Biol. 205:129-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATI MEDLINE-85124611; PubMed-2982499; Livneh E., Glazer L., Segal D., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hormone binding and kin Cell 40:599-607(1985).
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[2]
  STRAIN-Daekwanryeong;
                                                                                         Science
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Drosophila EGF receptor
one binding and kinase do
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(MAR-1998) to
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ignaling during photoreceptor
se, and null mutant Drosophila.";
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on of both
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     EMBL;
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"Interallelic complementation among DER/flb alleles: implications the mechanism of signal transduction by receptor-tyrosine kinases. Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Addresser Wall Represent Wall Wall Represent Wall Represent Represent Representation of the Representation of
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1 89:13-16(1997).

1 89:13-16(1997).

1 89:13-16(1997).

FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGUS, FUNCTION: BINDS TO FOUR LIGANDS: THE SIGNAL THROUGH THE RAS-RAF-WAPK PARTHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS. CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATE SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
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SUBCELLULAR LOCATION: ISOFORMS TO SUBCELLULAR LOCATION: ISOFORM TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND THORACIC AND ABDOMINAL GANGLIA.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE III, ARE PRODUCED BY ALTERNATIVE SPLICING.
TYSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF
TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
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                       AF052754; AAC08536.1;
AF052754; AAC08535.1;
AF052752; AAC08535.1;
K03054; AAA51462.1;
K03416; AAA51461.1;
AF109077; AAD26134.1;
AF109078; AAD26132.1;
AF109078; AAD26132.1;
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AF109079; AAD26133.1;
AF109079; AAD26133.1;
AF109079; AAD26133.1;
AF109080; AAD26133.1;
AF109081; AAD26133.1;
AF109081; AAD26133.1;
AF109083; AAD26133.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equires a license agreement email to license@isb-sib.ch
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AAD26133.1;
AAD26130.1;
AAD26130.1;
AAD26131.1;
AAD26131.1;
AAD26135.1;
AAD26135.1;
AAF46732.1;
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AND

PIR; A00640; GQFFE.

X02293; CAA26157.1; X78920; CAA55523.1; X78918; CAA55521.1; X78919; CAA55522.1;

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RESULT 15
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DT 01-OC
DT 01-OC
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PSI/4s;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Granulocyte-macrophage colony-stimulating fac
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BINDING
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Receptor; Phosphorylation;
Tyrosine-protein kinase; ATP-binding; Signal; Alternativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PROO109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
SMART; SM00261; FU; 7.
SMART; SM00219; TYRKC; 1.
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InterPro; IPR000719;
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PF00757; Furin-like; 1.
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Furin-like.
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BY SIMILARITY
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PROTEIN KINASE.
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EPIDERMAL GROWTH FACTOR RECEPTOR

EXTRACELLULAR (POTENTIAL).

POTENTIAL.
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InterPro; IRR000773; GM_CSF.
InterPro; IRR000773; GM_CSF; 1.
Pfam; PF01109; GM_CSF; 1.
PRINTS; PR00693; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
SMART; SM00040; CSF2; 1.
PROSITE; PS00702; GM_CSF; 1.
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Eukaryota; Metazoa; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytokine;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
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137
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FUNCTION: CYTOKINE THAT STIMULATES THE GROWTH AND DIFFEI
OF HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES,
GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES
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SUBUNIT: MONOMER (BY SIMILARITY).
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Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Ruminantia; Pecora; Cervoide
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Pred. No. 7.
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7.9e-23;
nes 19;
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ALIGNMENTS

RESULT 1 A24571

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A;Reference number: 157622; MUID:87286898; PMID:3039351 A;Accession: 157622 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <tal></tal>	A;Residues: 832-909 <rex> A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808 R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D. Mol. Cell. Biol. 7, 2597-2601, 1987 A.Title: Human HER2 (new) promoter: evidence for multiple mechanisms for transcription</rex>	A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma. A;Reference number: 159509; MUID:85272597; PMID:2992089 A;Accession: 159509 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA	A; Molecule type: mRNA A; Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <cou2> A; Cross-references: GB:M11730; NID:g183986 R; King, C.R.; Kraus, M.H.; Aaronson, S.A. Science 229, 974-976, 1985</cou2>	A;Accession: A44100 A;Molecule type: DNA A;Residues: 740-910 <coui> A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188</coui>	R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg Science 230, 1132-1139, 1985 A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chro A;Reference number: A44188; MUID:86070181; PMID:2999974	A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epic A;Reference number: A25491; MUID:86016729; PMID:2995967 A;Accession: A25491 A;Molecule type: DNA A;Residues: 737-1031 <sem> /sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem></sem>	A; Accession: A24571 A; Mccession: A24571 A; Mclecule type: mRNA A; Mclecule type: mRNA A; Residues: 1-1255 < YAM> A; Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 A; Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 A; Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 A; Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. R; Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985	protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein e C;Species: Homo sapiens (man) C;Date: 25-Oct-1987 *sequence_revision 06-Dec-1996 *text_charge 11-Jun-1999 C;Accession: A24571; A25491; A44188; B44188; I59509; I57622 C;Accession: A24571; A25491; A44188; B44188; IS9509; I57622 R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T Nature 319, 230-234, 1986 A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growt A. Beference number: A24571, MITD: 86118663. BMITD: 7003577

Оу 330 329	Db 556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	Оу 330 329	Db 496 TANRPEDECYGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECYEECRVLQGLPREYV 555	Qy 330 329	Db 436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCEVHTVPWDQLFRNPHQALLH 495	Оу 330 329	Db 376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 435	Оу 330 329	316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA	330	Db 256 LHENEGGICELHCPALVTYNTDTFESMPNPRGRYTRGASCYTACPYNYLSTDYGSCTLVC 315	196 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 2	QY 215 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 274	Db 136 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPC 195	Qy 155 GLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHDC 214	Oy 95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 154	Db 16 LPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 75	LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ 94	Query Match 64.3%; Score 2405.5; DB 1; Length 1255; Best Local Similarity 41.1%; Pred. No. 9.7e-126; Matches 509; Conservative 0; Mismatches 3; Indels 727; Gaps 1;	1139,1221,1222,1248/Binding site: phosphate (86/Binding site: phosphate (Thr) (covale	726-734/Region: protein kinase ATP-binding motif	676-1255/Domain: intracellular #status predicted 718-983/Domain: protein kinase homology <kin></kin>	395-605/Domain: EGF receptor extracellular domain repeat 654-675/Domain: transmembrane #status predicted <tmm></tmm>	70-304/Domain: E0	22-1255/Product: pi	, autophosphoryiation; dupiteation	pidermal growth factor receptor; protein kinase homology	r or fuctous is incombrete	Map postcion: 1/421.1-1/421.1 Introns: 25/1; 75/3; 147/1; 8	A;Gene: GDB:ERBB2; NGL; NEU: HER-2 A;Cross-references: GDB:120613; OMIM:164870	Comment: Ampirication and overexpression of this erbs-relations:	grences: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
;Reywords: ATP; autophosphorylation; duplication ;1-19/Domain: signal sequence #status predicted ;20-1260/Product: protein-tyrosine kinase neu #s	Gene Supe	A; Note: authors translated the codon GCA for residue 25 as val C; Genetics:	Residues: 637-663,'V',665-702 <was></was>	A; Status: preliminary		Carcinogenesis 12, 1975-1978, 1991 A;Title: Direct DNA sequencing of the rat new oncogene transmembrane domain reveals n	A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAAZ7059.1; PID:g56746 R;Masul, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohe	e type: mRNA	Reference number: A24562; MUID:86118662; PMID:3945311 Accession: A24562	19, 226-230, 1986	C;Date: 31:Dec-1988 #sequence_revision 31-Dec-1988 #text_change ii-Jun-1999 C;Accession: A24562; A61204 - R:Baramann, C T : Hung, M C : Weinberg, R.A.	-tyrosine kinase (EC 2.7.1.112) neu precursor - rat es: Rattus norvegicus (Norway rat)	Ν	DD 1210 AFDNJIYWDQDFFEKGAFFSTEKGIFTAENFEILGDDVF 1234	508 AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEXLGLDVP	440 PHERAKERGHILEKANILSPONGYYNDYEREGGAVENE 1156 PLPAARPAGATLERPKTLSPGKNGVYKDVFAFGGAVENPI	1096 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG	Qy 388 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 447	APGAGGMVHIRHRSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA	OV 330GAGGMVHUBBRSSGTRSGGGDI.TIGI.EDSSEGARDSDIADSSGAGGSDVEDGDI.GMGAA	Db 976 FSRMARDPORFVVTONEDIGPASPIDSTFYRSILEDDDMGDLVDAEEYLVPOOGFFCPDP	T Ov 330	916 MTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSE	330	856 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDV	ОУ 330 329	Db 796 LVTQLMPYGCLLDHVRENRGRLGSQDLLNNCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855	Оу 330 329	Db 736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795	Qy 330 329	Db 676 KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735	Qy 330 329.	Db 616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI 675

В	616	FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVVLGVVFGILI 675	575
Qy	330		329 .
В	676	KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 7	735
Qy	330		329
, B	736	KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGIÇLTSTVQ 7	795
VΩ	330		329
밁	796	${\tt LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS} \ \ \epsilon$	855
δ	330		329
Вb	856	PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVW3YGVTVWEL \$	915
Qy	330		329
В	916	MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE	975
Qy	330		329
Вb	976	FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP 1	1035
γQ	330		387
Db	1036	APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA	1095
Qy	388		447
В	1096	KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG	1155
Qγ	448		507
В	1156	PLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP	1215
Qy	508	AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546	
В	1216	AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254	

C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phos F;l-19/Domain: signal sequence #status predicted <SIG> F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>

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F:658-680/Domain: transmembrane #status predicted <TMN>
F:723-988/Domain: protein kinase homology <KIN>
F:731-739/Region: protein kinase ATP-binding motif
F:71.191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:691/Binding site: phosphate (Thr) (covalent) #status predicted
F:758/Active site: Lys #status predicted
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                          WCVQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKV
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SERLPQP 949 329 SEMDSTF 100 DLTLGLE 356 : ELTLGLE 106 ELTLGLE 106 ELTLGLE 106 ELTLGLE 106 :	;Residues: 1-1254 <res>;Cross-references: GB:D16295; NID:g493236; PIDN:BAA03801.1; ;Cross-references: GB:D16295; NID:g493236; PIDN:BAA03801.1; ;Cenetics: ;Gene: neu ;Gene: neu ;Superfamily: epidermal growth factor receptor; protein kina; ;Superfamily: epidermal growth factor receptor; protein kinase homology <kin>;736-734 Region: protein kinase Arp-hinding motif</kin></res>	R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M. Gene 140, 251-255, 1994 A;Title: Cloning and activation of the Syrian hamster new proto A;Reference number: I48161; MUID:94193007; PMID:7908275 A;Accession: I48161 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA		537 NPEYLGLDVP 1250 NPEYLGLDVP	477 1190	417 1130	357 1070	330 1010	950 P		890
):g747595 homology	Yamazaki, oncogene	1 —1		(GTPTAE 536 GTPTAE 1249.;	3GVVKDV 476 GVVKDV 1189	PLPSET 416	ELTLGLE 356	FMDSTF 1009	329	

Query Match Best Local S Matches 423 Local Sinhes 423; Similarity Conservative 51.8%; Score 1935; DB 2; 33.9%; Pred. No. 1.1e-99; tive 32; Mismatches 66; Length 1254; Gaps 2

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GPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTTCPYNYLS GPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLS

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TNRSRACPPCAPACKDNHCWGASPEDCQTLTGTIAPRAVPAARARLPTDCCHEQCAAGCT TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT

265 186 126

204 125

PTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNN 144

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145

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epidermal growth factor receptor precursor - chicken N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Gallus gallus (chicken) C;Date: 2B:Fcb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Accession: A27720; A00643
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RESULT 5
A42032
epidermal g
C; Species:

growth factor receptor - : Gallus gallus (chicken)

chicken

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F;31-1223/Product: epidermal growth factor receptor #status predicted <MAT>
F;31-654/Domain: extracellular #status predicted <EXT>
F;81-307/Domain: EGF receptor extracellular domain repeat <EE1>
F;97-610/Domain: EGF receptor extracellular domain repeat <EE2>
F;97-610/Domain: transmembrane #status predicted <TMM>
F;655-677/Domain: transmembrane #status predicted <TMM>
F;678-1223/Domain: intracellular #status predicted <INT>
F;717-984/Domain: protein kinase homology <KIN>
F;727-735/Region: protein kinase ATP-binding motif
F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent)
F;192,650/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte
F;754/Active site: Lys #status predicted
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #s
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A;Title: c-erbB activation in ALV-induced erythroblastosis: A;Reference number: A00643; MUID:85228222; PMID:2988784
A;Accession: A00643
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A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, express_A;Reference number: A27720; MUID:88261272; PMID:3260329
A;Accession: A27720.
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C;Genetics:
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A; Residues: 1-1223 <LAX>
A; Cross-references: GB: M20386
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A; Residues: 585-1223 <NIL>
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                                          SEGAGSDVFDGDLGMGAAKGLQSL
                                                                                                                                                                                  VPSDCCHNQCAAGCTGPRESDCLACRKFRDDATCKDTCPPLVLYNPTTYQMDVNPEGKYS
                                                                                                                                                                                                       LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT 309
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                                                                                         FGATCVRECPHNYVVTDHGSCV-----
                                                                                                                                   FGASCVTACPYNYLSTDVGSGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAP 369
                                                                                                                                                                                                                                                                         IDTSRK-PLTVLDFASNLSSCPKCHPNCTEDHCWGAGEQNCQTLTKVICAQQCSGRCRGK
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           A; Molecule type: mRNA
A; Molecule type: mRNA
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A; Residues: 1-1210 <ULL>
A; Residues: 1-1210 <ULL>
A; Residues: 1-1210 <ULL>
A; Rosidues: references: EMBL: X00588; NID: g31113; PIDN: CAA25240.1; PID: g757924
A; Rotos: The authors translated the codon AAG for residue 540 às Asn
A; Ishii, S:; Xu, Y:; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A; Title: Characterization and sequence of the promoter region of the human epidermal
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MOI. Cell. Biol. 12, 883-893, 1992
A;Title: An alternatively processed mRNA from the avian
A;Reference number: A42032; MUID:92123214; PMID:1732751
                                                                                                                                                                                                                                                                                                                                                      epidermal growth factor receptor precursor - N:Contains: protein-tyrosine kinase (EC 2.7.1
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                                                                                                                                                                                                                                             Nature 309, 418-425, 1984
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translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQCAAGCTGFKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTLID-TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YH-MNKTQ-----GLRELPMKRLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEITYVEHNRDLTFLKTIQEVAGYVLIALNMVDVIPLENLQIIRGNVLYDNSFALAVLSN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVLLLLLGRVALCS----AVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFLLFFWLDRSVLAKELARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQCAAGCTGPRESDCLACRKFRDDATCKDTCPPLVLYNPTTYQMDVNPEGKYSFGATCVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLTVLDFASNLSSCPKCHPNCTEDHCWGAGEQNCQTLTKVICAQQCSGRCRGKVPSDCCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                        ermal growth factor receptor cDNA sequence A00641; MUID:84219729; PMID:6328312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.28;
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Pred. No. 1.1
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2.7.1.112) erbB
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cches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---YEVEENGVRK-CKKCDGLCSK 345
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A;Residues: 1-29 <ISH>
A;Cross-references: GB.M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
R:Halev. J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Watu
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R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M. Oncogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identificatio A;Reference number: S30024; MUID:88217333; PMID:3329716

A; Accession: S30024

A; Molecule type: DNA A; Residues: 1-29 <HA2>

A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119

R; Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and A;Reference number: A38672; MUID:91107677; PMID:1988448
A;Accession: A38672

premature transcript termi

A; Molecule type: DNA A; Residues: 1-29 <HAL>

A; Cross-references: GB: M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A; Experimental source: carcinoma cell line A431-7
R; Xu, Y; Ishi, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.;
Nature 309, 806-810, 1984
A; Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RN
A; Teference number: A00642; MUID:84245835; PMID:6330563
A; Accession: A00642
A; Molecule type: mRNA
A; Residues: "RCAWRRA',150-187, 'KSVIQAV',195, 'M',197,'A',199-222,'S',224-304, 'RA',307A; Residues: "RCAWRRA',150-187, 'KSVIQAV',195, 'M',197,'A',199-222, 'S',224-304, 'RA',307A; PRESIdues: "RCAWRRA',150-187, 'KSVIQAV',195, 'M',197,'A',199-222, 'S',224-304, 'RA',307A; Residues: "RCAWRRA',150-187, 'KSVIQAV',195, 'M',197,'A',199-222, 'S',224-304, 'RA',307A; RESPECTATION CONTROL CONTRO

A;Title: Expression cloning of human EGF receptor complementary DNA: gene amplificati A;Reference number: A43615; MUID:84196372; PMID:6326261
A;Accession: A43615

A; Molecule type: mRNA A; Residues: 713-964 <LIN>

A;Experimental source: epidermoid carcinoma cell line A431 R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Cal Biochem. Biophys. Res. Commun. 124, 125-132, 1984 A;Reference number: A23062; MUID:85046483; PMID:6093780 A;Accession: A23062 Carpenter,

O'Malley,

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A; Molecule type: mRNA A; Residues: 1028-1210 <SIM> R; Weber, W; Gill, G.N.; Speiss, Science 224, 294-297, 1984

A; Reference number: A05281; MUID:84172183;

PMID:6324343

A;Accession: A05281 A;Molecule type: protein A;Residues: 25-30,'S',32

30,'S',32-51,454-467 <WEB>
Lukas, T.J.; Cohen, S.; St. S Staros, J.V.

R;Russo, M.W.; J. Biol. Chem.

J. Biol. Chem. 260, 5205-5208, 1985 A; Title: Identification of residues in the A; Reference number: A60143; MUID:85182650; nucleotide binding PMID:2985580 site of.

the

epidermal

factor receptor and

A;Reference number: A60143; MUID:85182650; PMID:298580
A;Accession: A60143
A;Accession: A60143
A;Molecule type: protein
A;Residues: 740-744, 'X', 746-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A;Title: ATP-stimulated interaction between epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth factor receptor an A;Title: ATP-stimulated interaction between Epidermal growth DNA Der,

Cell 59, 33-43, 1989
A;Title: Functional independence of the epidermal growth A;Reference number: A33331; MUID:90003233; PMID:2790960 factor receptor

annotation; internalization signa.

internalization

A;Contents: annotal C;Comment: Binding C;Genetics: of EGF to the receptor leads ç

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A; Gene: GDB: EGFR

A;Cross-references: GDB:120610; OMIM:131550 A;Map position: 7p12.3-7p12.1 C;Superfamily: epidermal growth factor receic;Keywords: ATP; autophosphorylation; dupli pidermal growth factor receptor; prautophosphorylation; duplication; protein kinuse homology
n; glycoprotein; phosphoprotein; phos

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F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1210/Product: EGF receptor #status predicted <ANT>
F:25-645/Domain: extracellular #status predicted <ANT>
F:75-300/Domain: EGF receptor extracellular domain repeat <EE1>
F:390-600/Domain: EGF receptor extracellular domain repeat <EE2>
F:390-600/Domain: transmembrane #status predicted <TMM>
F:646-668/Domain: intracellular #status predicted <TMM>
F:646-668/Domain: intracellular #status predicted <TMM>
F:710-975/Domain: protein kinase homology <KIN>
F:718-726/Region: protein kinase ATP-binding motif
F:999-1046/Region: coated-pit mediated internalization signal
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                                              Вb
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A;Title: Ligand-specific activation of HER4/p180erbB4, a fourth member A;Reference number: A47253; MUID:93189574; PMID:8383326
A;Accession: A47253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermal growth factor receptor, HER4 - human C;Species: Homo sapiens (man) C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999 C;Accession: A47253
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                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:L07868; NID:g337359; PIDN:AAB59446.1; A; Note: sequence extracted from NCBI backbone (NCBIP:126842)
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                                                                                                                                                                                                                                                                                                                                                                     A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                       :716-981/Domain:
                                                                                                                                                                                                                                                                          Superfamily: epidermal growth factor receptor; Reywords: ATP; growth factor receptor
                                                                                                                                                            Query Match
Best Local Similarity
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1047-1210/Region: inhibitory
128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status
745/Active site: Lys #status experimental
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                                                 7
TYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP 14:
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                                              LWVWVSLLVAAGTV-QPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVVMGNLEI 65
                                                                                        LFFWLDRSVLAKELARGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSL
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kinase ATP-binding motif
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41.5%; Pred. No. 7
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                                                                                                                                                            Score 721; DB 2;
Pred. No. 2.2e-32;
                                                                                                                                       Mismatches
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A;Cross-references: EMBL:Z12608
R;Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A;Title: Epidermal growth factor receptor threonine and A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermal growth factor receptor precursor - mouse
C;Species: Mis musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999,
C;Accession: A53183; A43818; S24942; A28941; S45325; 149643
R:Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenki
                                              A;Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA5: R;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K. R;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K. Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A;Title: Expression of the epidermal growth factor recept A;Reference number: I49643; MUID:93126380; PMID:7678348
                                                                                                                                                                                                                                                                                                                        R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S. submitted to the EMBL Data Library, April 1994 A;Description: The complete cDNA sequence of the A;Reference number: S45325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Eisinger, D.P.; Serrero, G. submitted to the EMBL Data Library, A;Reference number: S24942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givoncogene 6, 673-676, 1991
A;Title: Comparison of EGF receptor sequences as a guide A;Reference number: A43818; MUID:91232866; PMID:2030916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: The mouse waved-2 phenotype results from a point mutation A; Reference number: A53183; MUID:94170986; PMID:8125255 A; Accession: A53183
                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-971, 'K', 973-1210 <VER>
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A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-10
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A; Residues: 969-971, 'K', 973-1115, 'D'
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A; Residues: 1-714 <AVI>
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A; Residues: 1-12]
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A;Cross-references: GB:U03425
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S.K.
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A;Cross-references: GB:L06864; NID:g193001; FILM:AMANJULES...

A;Gene: EGFR
C;Gene: EGFR
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; kinase-related transforming protein; phosphoprotein signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <TMM>
F;712-977/Domain: transmembrane #status predicted <TMM>
F;712-977/Domain: protein kinase homology <KIN>
F;720-728/Region: protein kinase ATP-binding motif
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
F;997,Binding site: (or 1030 or 10312) phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: phosphate (Tyr) (covalent) #status experimental
F;1197/Binding site: phosphate (Tyr) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth factor receptor - rat (;Species: Rattus norvegicus (Norway rat) (;Species: Rattus norvegicus (Norway rat) (;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 10-Oct-1997 (;Accession: A36325 R;Petch, L.A.; Harris, J.; Raymond, V.W.; Blasband, A.; Lee, D.C.; Earp, H.; R;Petch, L.A.; Harris, J.; Raymond, V.W.; Blasband, A.; Lee, D.C.; Earp, H.; Mol. Cell. Biol. 10, 2973-2982, 1990 A;Title: A truncated, secreted form of the epidermal growth factor receptor A;Reference number: A36325; MUID:90258888; PMID:2342466
                                                                                                                                                                                                                                                        A;Cross-references: GB:M37394
A;Cross-references: GB:M37394
C;Superfamily: epidermal growth factor receptor; protein kinase
C;Keywords: alternative splicing; ATP; growth factor receptor
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A; Residues: 1-644 < PET>
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                                           ASLSFLODIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
                                                                                      LLAALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRN
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  YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAVLSN----
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46.8%; Pred. No. 3.1e-32;
tive 39; Mismatches 100;
                                                                                                                                                                             60;
                                                                                                                                                                           Score 714.5; DB 2;
Pred. No. 2.3e-32;
0; Mismatches 158;
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A;Title: Isolation and characterization of ERBB3, a third memb A;Reference number: A36223; MUID:90083234; PMID:2687875
A;Accession: A36223
                                                                                                                                                                                                                                                                                                                      C;Superfamily: unassigned Ser/Thr or Tyr-spec
C;Keywords: ATP; phosphotransferase
E;707-972/Domain: protein kinase homology <KI
F;715-723/Region: protein kinase ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-559,'G',561-957,'F',959-1063,'G',1065-1342 <
A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.
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A36223
A36223
Kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor -
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-No
C;Accession: A36223; I59164
R;Kraus; M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson. S.A.
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A;Cross-references: GDB:119880; OMIM:190151
A;Map position: 12q13-12q13
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A;Title: Molecular cloning and expression of another epidermal growth A;Reference number: IS9164; MUID:90311312; PMID:2164210
A;Accession: IS9164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1342 < KRA>
A; Cross-references: GB: M29366
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: unassigned Ser/Thr or Tyr-specific protein
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                      LAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIF
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                                                                  EVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFA
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                                                                                                                                                      -SLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERC
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Pred. No. 4.
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7;

hom

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A; Molecule type:
A; Residues: 18-21
C; Genetics:
                                                                                              A:Cross-references: GB:M10663; NID:g181145; PIDN:AAA52121.1; PID:g181146 A:Note: parts of this sequence, including the amino end of the mature prot R:Wen, D.Y.; Huang, B.R.; Cai, L.W.; J.Y. Acta Biochim. Biophys. Sin. 25, 651-655, 1993 A:Title: Amplification of human granulocyte-macrophage colony-stimulating A:Reference number: JC1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Cross-references: GB:M11734; NID:g181149; PIDN:AAA52122.1; PID:g181150 R;Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.; Luh, J.; Arai, K.; Re Proc. Natl. Acad. Sci. U.S.A. 82, 4360-4364, 1985 A;Title: Isolation of cDNA for a human granulocyte-macrophage colony-stimulating A;Reference number: A01853; MUID:85242684; PMID:3925454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
C;Accession: C24636; I59065; A25169; A01853; A44175; JC1090
R;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-144 <RES>
A;Residues: 1-144 <RES>
A;Cross-references: GB:M13207; NID:g181147; PIDN:AAA98768.1; PID:g181148
R;Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R
R;Cantrell, M.A.; Anderson, B2, 6250-6254, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 6250-6254, 1985
A;Title: Cloning, Sequence, and expression of a human granulocyte/macrophage colony-stir
A;Reference number: A25169; MUID:85298329; PMID:3898082
A;Accession: A25169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X03021; NID:g31858; PIDN:CAA26822.1; R;Kaushansky, K.; O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hag Proc. Natl. Acad. Sci. U.S.A. 83, 3101-3105, 1986 A;Title: Genomic cloning, characterization, and multilineage A;Reference number: I59065; MUID:86205844; PMID:3486413 A;Accession: I59065
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A;TILLE: Structure of the chromosomal gene
A;Reference number: A91015; MUID:86030234;
A;Accession: C24636
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N;Alternate names: colony-stimulating factor 2; GM-CSF
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                     A; Reference number: A44175; A; Accession: A44175
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-144 <LEE>
A;Cross-references: GB:M11220; NID:g183363; PIDN:AAA52578.1; PID:g183364
R;Wong, G.G.; Witek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary, A.C.; Lux
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                                                                                                                                                                                                                                                                                                                                                                                                      A.; Clark,
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A; Residues: 1-144 <CAN>
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A; Residues: 1-144 <MIY>
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                                                                                                                                                                                                                                                                                                                                                                               Science 228,
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                    :ype: protein
18-21,'C',23-96,'L',98-144 <WEN>
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Segal, G.M.; Hagen, F.S.; A
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118
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1339 < HELD
A; Cross-references: GB:U29339; NID:g915389; PID:g915390
A; Experimental source: liver
A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue A; Note: The authors translated the codon AAC for residue A; Note: The authors translated the codon AAC fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F:640-659/Domain: transmembrane #status predicted <TMM>
F:705-709/Domain: protein kinase homology <KIN>
F:713-721/Region: protein kinase APP-binding motif
F:733-721/Region: protein kinase APP-binding motif
F:939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Kol
Gene 165, 279-284, 1995
A:Title: Cloning of the rat ErbB3 cDNA and characterization
A;Reference number: JC4387; MUID:96096535; PMID:8522190
A;Accession: JC4387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: stimulates the differentiation and proliferation of hematopoietic C;Superfamily: granulocyte-macrophage colony-stimulating factor C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status experi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:CSF2
A;Cross-references: GDB:119812; OMIN:138960
...man position: 5q23.2-5q31.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: ATP; growth factor receptor; liver; phosphoprotein; trans
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1339/Product: epidermal growth factor homolog #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase C;Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth factor receptor homolog precursor N;Alternate names: ErbB3 protein; HER3 protein C;Species: Rattus norvegicus (Norway rat) C;Date: 17-Jan-1996 #sequence_revision 19-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;44,54/Binding site: carbohydrate (Asn) (covalent) #status
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134 AVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH 193
                                                                                                                                                                                                                      74 VVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYAL
                                                                                                                                                                                                                                                                                                                                                                                                   17 GFLFLLFFWLDRSVLAKELARGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQ
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                                                                                                                                                                                                                                                                                                                                          GTLQVLCFLL-----SLARGSEMGNSQAVCPGTLNGLSVTGDADNQYQTLYKLYEKCE
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Pred. No. 4.2e-29;
4; Mismatches 108;
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RESULT 13

$06142

$06142

$06142

protein-tyrosine kinase (EC 2.7.1.112) mrk-y precursor - southern platyfish N;Alternate names: epidermal growth factor receptor homolog; kinase-related C;Species: Xiphophorus maculatus (southern platyfish)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000 C;Accession: $06142; $13809

C;Accession: $06142; $13809

R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;CLOSS ACCURENCE A;Aldam, D.; Maeueler, W.; Schart, P., Oncogene 6, 73-80, 1991
Oncogene 6, 73-80, 1991
A;Title: Transcriptional activation of the number: S13807; MUID:91125882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1166 <WIT>
A; Cross-references: EMBL: X16891; NID: g65290;
A; Cross-references: W; Schartl, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F; 26-1166/Product:
F; 707-972/Domain:
F; 715-723/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C:Superfamily: epidermal growth factor receptor; protein kinase homology C:Keywords: ATP; growth factor receptor; phosphotransferase; transmembran F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-1166/Product: kinase-related transforming protein (Tu) #status pred: F:707-972/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A;Residues: 821-1025,'N',1027-1098,'A',1100-1166 <ADA>
A;Residues: 821-1025,'N',1027-1098,'A',1100-1166 <ADA>
A;Residues: B21-1025,'N',1027-1098,'A',1100-1166 <ADA>
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A; Introns: 872/3;
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A; Accession: S13809
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Best Local
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                         TCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAACVKECPSNYVVTE---
                                                CWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSG
                                                                                                                                                                                                      NLTEILSGGVKVSHNPLLCNVETINWWDIVDKTSNPTMNLIPHAFERQCQKCDHGCVNGS
                                                                                                                                                                                                                                                                                          VLIAMNEVSTIPLVNLRLIRGQNLYEGNFTLLVMSNYQK-NPSSP--DVYQVGLKQLQLS 143
                                                                                                                                                                                                                                                                                                                                         VLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR 162
                                                                                                                                                                                                                                                                                                                                                                                KVCQGTSNQMTM----LDNHYLKMKKMYSGCNVVLENLEITYTQENQDLSFLQSIQEVGGY
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                                                                                                                                                                                                                                             SLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
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Pred. No. 8.2e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
A61632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:X53561; NID:g1800; PIDN:CAA37632.1; PID:g1801 C;Comment: This protein is a glycoprotein cytokine produced and secreted by va. C;Superfamily: granulocyte-macrophage colony-stimulating factor C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-ceil F;1-17/Domain: signal sequence #status predicted <SIG> F;1-17/Porduct: granulocyte-macrophage colony-stimulating factor #status predicted F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                A;Cross-references: GB:X55991; NID:g6983759; PIDN:CAA39463.1; C;Superfamily: granulocyte-macrophage colony-stimulating factor F;1-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 105, 275-279, 1991
A;Title: Cloning and expression of a cDNA encoding ovine A;Reference number: JH0469; MUID:92039044; PMID:1937025
A;Accession: JH0469
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A;Title: Cloning and sequencing of the cDNA for A;Reference number: A61632; MUID:91331592; PMID:
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A; Residues: 1-144 <MCI>
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A; Residues: 1-144 < OAB>
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Best Local Similarity
                                                                                                               548 AAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 607
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                                                                                                                                                                                                   Local Similarity
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                     ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 667
                                                                                        SAPTRQPSPVTRPWQHVDAIKEALSLLNDSTDTAAVMDETVEVVSEMFDSQEPTCLQTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF
ELYKQGLRGSLTSLTGSLTMMASHYKKHCPPTQETSCETQ11TFKSFKENLKDFLF11PF
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279, 1991
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Pred. No. 1.1e-23;
1; Mismatches 16
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Gaps

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Gaps

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Oy 668 DCWEPPVQE 675
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Db 137 DCWEPAQK 144

Search completed: April 28, 2003, 13:42:22
Job time: 32.3846 secs

Copyright

GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.

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Database
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Listing first 45 summaries
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1 MRAAPLLLARAASLSLGFLF.....EPVQEGAPPPPAAAHHHHHH 690
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001
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1660.081 Million cell updates/sec
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and is derived by a Pred. No. is the number of results predicted by chance to later than or equal to the score of the result being the dealysis of the total score distribution chance to have result being pu printed,

Result No.	Score	Query Match	Query Match Length DB	BB	ID	Description
–	3739		690	22	AAE13109	Human HER500-hGM-C
2	3473.5	92.9	697	22	AAE13111	Human HER500-rGM-C
ω	2972	79.5	555	22	AAE13108	Human HER500 fusic
4	2957.5	79.1	564	22	AAE13110	Human HER500 fusic
₅	2573.5	68.8	919	21	AAB21203	Human HER-2/neu fu
0	2573.5	68.8	919	23	AAM51148	Her-2/neu extracel
7	2410.5	64.5	1255	21	AAY92620	Human heregulin 2
8	2410.5	64.5	1255	22	AAE12130	Human tyrosine kir
9	2410.5	64.5	1255	22	AAB60167	HER2 transgene pla
10	2410.5	64.5	1255	23	AAU74545	Human HER2 (ErbB2)

5	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
1551	1551	1551	1553	1562	1587	1612	1612	1612	1612	1612	1612	1628.5	1948	1948	1961	1961	1961	2092.5	2129	2130	2188.5	\sim	•	•		•	•	•	•	•	•	405.	2405.5	405.
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AAE09200	AAE09183	AAE09181	AAE20348	AAR08222	AAE13120	AAM51149	AAB21204	AAM51145	AAB21200	AAB61593	AAB60408	AAY44993	AAM51144	AAB21199	AAM51151	AAG62860	AAB21206	AAB21208	AAM51152 ·	AAM51153	AAE13112	AAW19764	AAU98923	AAR39568	AAU77114	AAM51143	AAE20479	AAE24067	AAG88267	AAB85458	AAY84780	AAB21198	AAW92406	AAW01111
		Human p68HER-2 gen	Human truncated HE	Extracellular port	Mature human HER-2	Her-2/neu extracel	Human HER-2/neu fu	Human Her-2/neu on	Extracellular HER-	Human ErbB2 extrac	0	DC8scFv-erbB2EC fu	Rat Her-2/neu onco	Rat MER-2/neu prot	Mouse Her-2/neu on	acid seque		HER-2/neu	Her-2/neu	Mouse Her-2/neu ex	HER300	٠.	east	f c-er	Her-2/neu	Her-2/neu	Her-2/	Her-2 pro	neu amino a	N	acid seque		-2/neu	HER-2/neu protein.

ALIGNMENTS

28-JAN-2002 (first entry) AAE13109; AAE13109 standard; Protein; 690 AA. Human HER500-hGM-CSF fusion protein construct.

Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; pap protein; Ala Arg linker; membrane distal extracellular domain; PAP protein; Ala Arg linker; membrane distal extracellular domain; C-terminal tag; human; GM-CSF; membrane distal intracellular domain; C-terminal tag; human; GM-CSF; HER-2 protein; granulocyte-macrophage colony stimulating factor; HER-500-hGM-CSF fusion protein.

Chimeric -Homo sapiens. Synthetic.

WO200174855-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US10515.

30-MAR-2000; 2000US-193504P

(DEND-) DENDREON CORP.

Laus R, Vidovic D, Graddis T;

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Claim
                                                                                       2001-662965/76.
DB; AAD21565.
7; Page 26; 59pp; English.
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XXCCCCCCCCCCCCXXXXPT9XXX

immunostimulatory fusion protein comprising the intracellular domain HER-2 and an antigen elicits an immune response to the antigen and useful for the treatment of associated cancer associated - $\,$

The invention relates to immunostimulatory fusion proteins (IFP) and conclete acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 hGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains, an Ala Ala linker, a mature human granulocytemacrophage colony stimulating factor (GM-CSF) sequence and a C-terminal tag. is HER500 cellular derived

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Sequence 690 Ą

Query Match Matches

Local

Similarity

100.0%; 0;

Score 3739; DB 22; Pred. No. 4.8e-226; Mismatches

0

Indels Length

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Conservative

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                                                            LGLDVPAAAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEP
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Query Match Best Local S Matches 641

Similarity

92.98;

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                           nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 rGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature PAP protein, an Ala Arg linker, an ovalumin (oVA)-derived immunodominant octapeptide, an Ala linker, an ovalumin (oVA)-derived immunodominant octapeptide, tar granulocyte-macrophage colony stimulating factor (GM-CSF) sequence and a C-terminal tag.
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          30-MAR-2001; 2001WO-US10515
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                                                                                    HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                            Cheever MA,
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                                                                                                                                                                                                                                                                                       Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                  breast cancer;
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                                                                                                                                                                                                 29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                            HER-2/neu; oncogene; tyrosine kinase;
                                                                                                                                                                 CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                            Gheysen
                                                                                                                                                                                                                                                                                                                     ; prostate cancer; ovarian cancer; fusion protein.
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The present sequence is a fusion protein comprising the extracellular domain and the phosphorylation domain of the human HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor recept

Claim 2; prostate

Fig 12; 128pp;

English

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Matches
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                                                                                                                                                            RSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPL 423
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ENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGL
                   ENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGL 543
                                                                                                                                                                                                                                                DDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP
                                                                                                                                                                                                                                                                                                                               FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSQNEDLGPASPLDSTFYRSLLED
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56.4%;
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Pred. No. 7.1e-153;
D; Mismatches 3;
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                     The present sequence is that of a fusion protein between the cextracellular domain and phosphorylation domain of human Her-2/neu (see AAM5143), an oncogenic self-protein and target for anti-cancer cx vaccines. The fusion protein can be obtained by recombinant DNA cmethods. Her-2/neu overexpression correlates with a poor prognosis cin breast and ovarian cancers. The invention provides Her-2/neu cx vaccines comprising the fusion proteins or nucleic acids encoding them, viral vectors, and cx vaccines comprising the fusion proteins or nucleic acid molecules. CIn preferred fusion proteins, the extracellular domain of a cx vaccines comprising the fusion proteins or nucleic acid molecules. CIn preferred fusion proteins, the extracellular domain or phosphorylation domain (or its Deltapp fragment). An immune cx phosphorylation domain (or its Deltapp fragment). An immune cx cadministering the fusion protein in the form of a vaccine, or by cx caministering the fusion protein in the form of a vaccine, or by cx caministering the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated concer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu corder to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-)
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                                                                                                                                                                                                                                                                                                                                                                                           Claim 2;
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inase; receptor; c-erbB2; gene therapy.
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                   AAY92620 standard; Protein;
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                                                                                          DVP 546
                                                                                                                       ENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGL
                                                                                                                                                           TCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
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20-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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LHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC
LHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC
                                                                                                                                         SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                     DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 154
                PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375
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98US-0105011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGF8b and Her2, respectively.
                                                                                                                                                                                                                                                                                                                                                                                          Score 2410.5; DB 21; Length 1255; Pred. No. 1.7e-142; 0; Mismatches 2; Indels 727; Gaps
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   Therapeutic compound; major histocompatibility complex; vaccine; antigenic peptide; MHC; immunoregulatory; immune response; HER-2;
                                             Human tyrosine kinase-type receptor, HER-2
                                                                              18-DEC-2001
                                                                                                                                         AAE12130 standard; Protein; 1255
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		ULT 8	AAE:
	AFDNLXYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254	1216	DЬ
	AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546	508	Q
1215	PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP	1156	Ф
507	aarpagatleraktlspgkngvykdyfafggavenf	448	Qy
1155	Ç) -	1096	Db
447		388	Qy
1095	APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA	1036	DЬ
387	GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDI,GMGAA	330	Qy
1035	FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP	976	Db
329		330	Qy
975	MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECKPRFRELVSE	916	В
329;		330	Qy
915	PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL	856	Db
329		330	Qy
855	LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS	796	Db
329		330	Qy
795	KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ	736	Вb
329		330	δĀ
735	KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY	676	В
329		330	δĀ
675	${\tt FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILI}$	616	밁
329		330	Qy
615	NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMP1WK	556	В
329		330	Ωу
555	TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV	496	B
329		330	Qy
495	LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH	436	Вb
329		330	Qγ
435	FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI	376	망
329		330	Qy

(first entry)

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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Compounds that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of gene transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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Matches 510; Conserv
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Region
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N-PSDB; AAD19731.
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antigen presenting cell; human; tyrosine kinase-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                  DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG
                                                                                                                       SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCCHEQCAAGCTGPKHSDCLAC
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                                                                                                                                                                                                                                                                                                                                          LPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ
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                                                                                                   SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
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Pred. No. 1.7e-142;
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                                                                                                                                                                                                                      AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. particular, the antibody is directed against ErbB2 (also known as HE) and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating tumors, particularly breast cancers, receptor and does not respond to an anti-ErbB conjugating the antibody to a maytansinoid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HER2
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16-MAR-2000; 2000US-0189844.
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DB; AAF24297.
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Pred. No. 1.7e-142;
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                    Human; HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ova stomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; glaid disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder;
                                                                                                                                                                                                                       Human HER2 (ErbB2) polypeptide.
                                                                                                                                                                                                                                                                              23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                              AAU74545
                                                                                                                                                                                                                                                                                                                                                                              standard;
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В	436	LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495	
Qy	330	329	
Ф	496	TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGI,PREYV 555	
Qy	330	329	
Дb	556	NARHCLPCHPECOPONGSVTCFGPEADOCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615	
Qy	330	329	
DЬ	616	FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILI 675	
Qy	330	329	
日	676	KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY 735:	
Qy	330	329	
В	736	KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ 795	
Qy	330	329	
Ф	796	LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855	
Qy	330	329	
Дb	856	PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL 915	
Qy	330	329	
ф	916	MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSE 975	
Qy	330	329	
В	976	FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLYPQQGFFCPDP 1035	
Qy	330	GAGGMVHHRHRSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 387	
Вb	1036	APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA 1095	
Qy .	388	KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 447	
Db	1096	KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 1155	
Qy	448	PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP 507	
Db	1156	PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP 1215	
Qγ	508	AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546	
В	1216	AFDNLYYMDQDPPERGAPPSTFKGTFTAENPEYLGLDVP 1254	
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Best Local Similarity 41.2%;
Matches 510; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating tumour characterised by overexpression of epidermal factor receptor, ErbB or cancer in mammal, comprises administanti-ErbB antibody-maytansinoid conjugate to the mammal
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05-OCT-2000; 2000US-238327P.
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(SCHW/) SCHWALL R.
(SLIW/) SLIWKOWSKI M.
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                          PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA
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                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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Pred. No. 1.7e-142;
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HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; immunisation; tumour; vaccine; vector.
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                                                HER-2/neu protein
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                                                                                                                                                                                                                                            KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG
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Best Local Similarity 41.1%;
Matches 509; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AA740739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector
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Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding HER-2-neu poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/\text{neu} oncogene is associated
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                that directs expression of the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 56-61; 71pp; English.
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N-PSDB; AAT40739.
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376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI 435
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                                                                                                  SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
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                                                 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375
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/note= "claimed domain, useful for immunisation"
                                                                                                                                                                                                                                                                                                                                                               Score 2405.5; DB 17; Length 1255;
Pred. No. 3.5e-142;
0; Mismatches 3; Indels 727; Gaps
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gnancy; treatment; tumour. saplens.	mali Homo	XOXXX
HER-2/neu oncogene protein.	n a	XX
APR-1999 (first entry)	21-A	ΧŻ
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)2406 standard; Protein; 1255 AA.	ULT 12 92406 AAW9	RES AAW ID
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GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSBGAGSDVFDGD	330	Qy
FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFC	976	Д
	330	Qy
MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRE	916	DЬ
	330	Qy
PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWE	856	DЬ
	330	Qy
LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVK	796	В
	330	Q
KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLT	736	Дb
	330	Qy
KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAF	676	рb
	330	Qy
FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFG	616	Ф
	330	Qy
NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMP	556	ф
	330	, Qy
TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV	496	망
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Location/Qualifiers

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Matches 509; Conservative
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17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of HER-2/neu polypeptides - for eliciting an immune response to an HER-2/neu associated malignancy, particularly for treating or preventing tumours
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N-PSDB; AAX01912.
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436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH 495
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                                                    FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI
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93US-0033644.
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95US-0414417.
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/note= "region which elicits immune response"
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	16 AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254	Db 121	
	108 AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546	Ωу 5	
1215	6 PLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP	Db 115	
507	PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP	Оу 448	
1155	6 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG	Db 109	
447	88 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG	∵.Qy 36	
1095	APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVEDGDLGMGAA	Db 1036	
387	0GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA	Qу 33	
1035	FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP	Db 976	
329	330	0у 3:	
975	916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRERELVSE	Db 9:	
329	330	Qy 3:	
915	6 PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL	28 qd	
329	330	Qy 3:	
855	796 LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS	Db 79	
329	330	Qy 3:	
795	KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ	Db 736	
. 329		Qу 330	
735	676 KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY	Db 67	
329		Qу: 330	
675	FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI	Db 616	
329	330	0у з:	
615	6 NARHCLPCHPECOPONGSVTCFGPEADOCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK	Db 55	
329	330	0у 3:	
. 55	496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV	Db 45	
329	330	οу 3;	

RESULT 13 AAB21198

AAB21198 standard; protein; 1255 ₿

12-JAN-2001 (first entry)

Human HER-2/neu protein

Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; breast cancer; prostate cancer; ovarian cancer; lung cancer; colon cancer.

Homo sapiens.

WO200044899-A1

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Best Local Similarity 41.1%;
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N-PSDB; AAA89736.
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SMITHKLINE BEECHAM
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Pred. No. 3.5e-142;
0; Mismatches 3;
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NO.00000579-A1.	E erbB-2 receptor protein; cell transformatic cell proliferation; tissue degeneration; art resorption; inflammatory disease; degenerativ healing.		80 standard; Protein; 1255 AA.	AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 546	PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEXLTPQGGAAPQPHPPPAFSP 507 	KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 447	GAGGMVHHRHRSSSTRSGGGDLTLGLEPSBEEAPRSPLAPSBGAGSDVFDGDLGMGAA 387 	FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP 1035		MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSBCRPRFRELVSE 975	nhvkttdfglarlldideteyhadggkvpikwmalesilrrffthqsdvwsygvtvwel	329	LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKS 855	329	KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICITSTVQ 795	329	KRRQQKIRKYTMRRLLQETELVEPLTPSGAMENQAQMRILKETELRKVKVLGSGAFGTVY 735	329	FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI 675	329	NAKHCHECHEECQEQNGSYICEGEEADQCYACAHIADEEECYARCESGYAEDDSIMEIMA 013
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Best Local Similarity 41.1%;
Matches 509; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
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N-PSDB; AAA14812.
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                              NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK 615
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                                                                                           TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV
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40 AG	676 KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETE 330 3736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAVVMAGVGS
70 dd 40	330
g g	736 KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVS
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5	Оу 330
, Dp	Db 796 LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLV
Qy	Оу 330
рь	Db 856 PNHVKITDEGLARLLDIDETEYHADGGKVPIKWMALESILRRRETHQSDVWS
Qy	Оу 330
рь	Db 916 MTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSEC
Qy	Оу 330
В	Db 976 FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLV
Qy	330GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAP
рь	Db 1036 APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGA
Qy	388 KGLQ
ф	1096 KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQ
Qy	QY 448 PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAA
₽	1156 PLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGG
Qy	508 AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
₽	1216 AFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLC
RESI	RESULT 15
X II	- 1
ž č	AC AAB85458;
Y D ?	DT 25-SEP-2001 (first entry)
Y D ?	DE Human HER-2/neu protein.
K K K	KW Antigen-presenting cell; immunogenic; immune response KW oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.
80	OS Homo sapiens.
Y P S	PN W0200153463-A2.
K B S	PD 26-JUL-2001.
Y P S	PF 19-JAN-2001; 2001WO-US01850.
Y P R	PR 21-JAN-2000; 2000US-0177545.
X P X	PA (CORI-) CORIXA CORP.
YY	PI Cheever MA, Hand-Zimmermann S;
DR DR	DR WPI; 2001-476112/51. DR N-PSDB; AAH23392.

	329	330	δ
19.	735	676 KRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVY	Db
	329	330	Qy
	675	616 FPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLVVVLGVVFGILI	90
	329	330	Qγ
	615	556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWK	DЬ
	329	330	Qy
	555	496 TANRPEDECYGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECYEECRYLQGLPREYY	В
	329	330	Qy
	495	436 LHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLH	DЪ
	329	330	Qy
	435	376 FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRI	В
	329	330	οy
	375	316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA	Дb
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•	329	275 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGS	γo
	274 255	215 SPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAC	B 9
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	214	155 GLRELOLRSLTEILKGGVLIORNPOLCYODTILWKDIFHKNNOLALTLITYTNRSRACHDO	9
	154 135	95 DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPG 	Оy
	94 75	35 LARGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ	g. Q
	aps 1;	Query Match 64.3%; Score 2405.5; DB 22; Length 1255; Best Local Similarity 41.1%; Pred. No. 3.5e-142; Matches 509; Conservative 0; Mismatches 3; Indels 727; Ga	3 0 0
.•		Sequence 1255 AA;	SQ
•	es í	eful as vaccines for eliciting or enhancing an immune response R-2/neu protein, particularly in treating or preventing maligich the HER-2/neu oncogene is associated. Specifically, these eful for treating or preventing cancer, e.g. breast cancer, or lon, lung or prostate cancers. The present sequence represents e human HER-2/neu protein (also known as p185 or c-erbB2).	888888
	ch produces cells are	<pre>ides an isolated antigen-presenting cell, whice immunogenic portion of a polypeptide that to HER-2/neu protein. The antigen-presenting</pre>	8888
		Claim 2; Page 41-46; 49pp; English.	PS
	seful	New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly us for treating or preventing cancer, e.g. breast cancer	Tq Tq
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PLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP
PLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSP
KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG
KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG
APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA
-GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAA
FSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP
mtfgakpydgipareipdllekgerlpqppictidvymimvkcwmidsecrprfrelvse
PNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWEL
LVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQTAKGMSYLEDVRLVHRDLAARNVLVKS
KGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQ

Search completed: April 28, 2003, 13:39:43 Job time: 72.3846 secs

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ALIGNMENTS

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A;Gene: neu
C;Superfamily: e
C;Keywords: ATP
F;718-983/Domain
                                                                                                                                                                                                                                                                          Gene 140, 251-255, 1994
A;Title: Cloning and activation of the Syrian hamster neu A;Reference number: 148161; MUID:94193007; PMID:7908275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F:395-605/Domain: EGF receptor extracellular domain repeat <EE2>
F:654-675/Domain: transmembrane #status predicted <TMM>
F:654-675/Domain: intracellular #status predicted <IMM>
F:676-1255/Domain: intracellular #status predicted <IMT>
F:718-983/Domain: protein kinase homology <KIN>
F:726-734/Region: protein kinase ATP-binding motif
F:686,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:753/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 17q21.1-17q21.1

-A;Introns: 25/1; 75/3; 147/1; 883/3

A;Note: the list of introns is incomplete
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                                                                                                                                                                                                                                                                                                                                                                 p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: I48161
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                                                                          F;718-983/Domain:
F;726-734/Region:
                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-1254 < RES>
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F;2-1255/Product: protein-tyrosine kinase erbB2 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OM
                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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      Matches
                      Query Match
Best Local :
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Best Local
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70-304/Domain: EGF receptor extracellular domain repeat <EE1>
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251-255,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF
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                    Similarity
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                                                                                                                                     epidermal
                                                                                                                                                                                                                                                                                                                                                   Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki,
                                                                          protein
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                             GB:D16295; NID:g493236; PIDN:BAA03801.1;
                                                                                                                                     growth factor receptor;
                                                                            kinase
kinase
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                    81.8%;
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ATP-binding
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  Pred. No. 8.1
3; Mismatches
                    Score 966.5;
Pred. No. 8.
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3.1e-56;
hes 25;
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A; Residues: 637-663, 'V', 665-702 <MAS>
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                                                                                                                   1103
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                                                                                                                                                                                                                                                                                            Local
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                                                                                                                 LOSLSPHDLSPLORYSEDPTLPLPPETDGYVAPLACSPQPEYVNQSEVQPQPPLTPEGPL 1162
                                    PPVRPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLVPREGTASPPHPSPAFSPAF
                                                            PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF 180
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                        80.7%;
81.6%;
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C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorylation; diplication; glycoprotein; phosphorylation; protein-tyrosine kinase neu *status predicted <MAT> F;20-1260/Product: protein-tyrosine kinase neu *status predicted <TMN> F;21-730-988/Domain: protein kinase homology <KIN> F;731-739/Region: protein kinase ATP-binding motif F:711-739/Region: protein kinase ATP-binding motif F:71,191,263.535,576,634/Binding site: carbohydrate (Asn) (covalent) *status predicted F;758/Active site: Lys *status predicted F:758/Active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Residues: 1-1260 <BAR>
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R;Masul, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith
Carcinogenesis 12, 1975-1978, 1991
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane dome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-thlazolyl]formamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063
A;Accession: A61204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: authors translated the codon GCA for residue
                                                                                                                             1038 GAGSTAHRRHRSSSTRSGGGELTLGMEPSGEEPPRSPLAPSEGAGSDVFEGELGMGATKG
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                                                                                                                                                                                                                                                                                                               Score 954; DB 1;
Pred. No. 5.4e-55;
8; Mismatches 32;
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R; Weber, W.;
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A; Reference n
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A:Molecule type: mRNA
A:Residues: 1-1210 <ULL>
A:Residues: 1-1210 <ULL>
A:Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A:Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A:Note: the authors translated the codon AAG for residue 540 as Asn
A:Note: the authors translated the codon AAG for residue 540 as Asn
R:Ishi1, S:; Xu, Y:; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R;Haley, J.D.; Waterfield, M.D.
J. Blol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and premature transcript terminat A;Reference number: A38672; MUID:91107677; PMID:1988448
A;Accession: A38672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272 R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Watt Oncogene Res. 1, 375-396, 1987 A;Title: The human EGF receptor gene: structure of the 110 kb locus and A;Reference number: S30024; MUID:88217333; PMID:3329716
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                                                                                                                                                                                           A; Reference number: A23062;
                                                                                                                                                                                                                             R;Simmen, F.A.; Gope, M.L.; Sci
Riochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 713-964 <
                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Expression cloning of human EGF receptor complementary DNA: gene A;Reference number: A43615; MUID:84196372; PMID:6326261 A;Accession: A43615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Lin, C.R.; Chen, W.S.; Ki
Science 224, 843-848, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: RCAWRRA, 150-187, KSVIQAV, 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-321 ', 798-799, 'TD', 802-811, 'R', 813-942 <XUV>
R;Experimental source: A431 human caroinoma cells, which have large numbers of EGF recept R;Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Human epidermal growth factor receptor cDNA is homologous A;Reference number: A00642; MUID:84245835; PMID:6330563 A;Accession: A00642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PII
A;Experimental source: carcinoma cell line A431-7
R;Xu, Y; Ishi1, S; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.;
Nature 309, 806-810, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-29 <HA2>
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                                                                                                 A; Molecule type: mRNA
A; Residues: 1028-1210 <SIM>
                                                                                                                                                                 A; Accession: A23062
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A;Residues: 1-29 <ISH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
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                              W.; Gill, G.N.;
224, 294-297, 198
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   A05281; MUID:84172183;
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M.L.; Schulz, T.Z.; Wright, D.A.; Ca
                                                               Speiss,
                                                                                                                                                                                        Schulz, T.Z.; Wi
un. 124, 125-132,
MUID:85046483; [
   PMID: 6324343
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A; Residues: 25-30, 'S', 32-51;454-40, S.; Staros, J.V.
R; Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A; Title: Identification of residues in the nucleotide binding A; Reference number: A60143; MUID:85182650; PMID:2985580
A; Accession: A60143
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A;Gene:
                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Stecies: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence revi
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A;Title: Functional independence of the epidermal growth factor rec
A;Reference number: A33331; MUID:90003233; PMID:2790960
A;Contents: annotation; internalization signal
C;Comment: Binding of EGF to the receptor leads to internalization
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                               R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; (Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993)
A;Title: Ligand-specific activation of HER4/p180e
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F;128,175,352,413,444,528,603/Binding site:
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F;718-726/Region: protein kinase ATP-binding motif
F;999-1046/Region: coated-pit mediated internalization signal
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F;646-668/Domain: transmembrane #status predicted <TMN>
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A;Map position: 7p12.3-7p12.1
C;Superfamily: epidermal growth
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A; Residues: 740-744, 'X', 746-747 < RUS>
A;Reference number:
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75-300/Domain: EGF receptor extracellular domain repeat 
390-600/Domain: EGF receptor extracellular domain repeat
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Residues: 25-30
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Pred. No. 0.0026;
4; Mismatches 69
                                   HER4/p180erbB4,
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A;Accession: A47253
A;Status: preliminary; not compared with conceptual translation
A;Rolecule type: nucleic acid
A;Residues: 1-1308 <PLO>
A;Residues: 1-1308 <PLO>
A;Cross-references: GB:LO7868; NID:g337359; PIDN:AAB59446.1; PID:g337360
A;Note: sequence extracted from NCBI backbone (NCBIP:126842)
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
F;716-981/Domain: protein kinase homology <KIN>
F;724-732/Region: protein kinase ATP-binding motif
                                                                                            A:Map position: 4q-4q
C;Superfamily: unassigned ribonucleoprotein repeat-containing
C;Keywords: alternative splicing; pre-mRNA splicing; surface a
F;298-359/Domain: ribonucleoprotein repeat homology <RRM1>
F;372-438/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: A46302; A43557; S29995
R:Patton, J.G.; Porro, E.B.; Galceran, J.; Tempst, P.; Nadal-Ginard, B. Genes Dev. 7, 393-406, 1993
                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 312-707 <GOW>
A; Cross-references: GB: X16850;
                                                                                                                                                                                                                                                                                                                                                                                A;Title: Cloning and characterization of a myoblast cell surface A;Reference number: A43557; MUID:90091812; PMID:2480877 A;Accession: A43557
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X70944; NID:g38457; PIDN:CAA50283.1; PID:g38458 A;Note: sequence extracted from NCBI backbone (NCBIP:127206) R;Gower, H.J.; Moore, S.E.; Dickson, G.; Elsom, V.L.; Nayak, R.; Walsh, Development 105, 723-731, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
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A; Residues: 1-707 <PAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Cloning and characterization of PSF, a novel pre-mRNA splicing A; Reference number: A46302; MUID:93194059; PMID:8449401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTB-associated splicing factor, long form - human N; Alternate names: myoblast cell surface antigen
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                                                                                                                                                                                                                                           A; Gene: GDB:SFPQ; PSF
                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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                          Best
    Matches
                                                Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDGGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCNGTLRKPVAPHVQEDSSTQ 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTFANTLGKAEYLKNNILSMPEKAKKAFDNPDYWNHSLPPRSTLQHPDYLQEYSTKYFYK 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PPKAEDEYVNEPLYL 1209
  58; Conser
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                        12.3%;
26.6%;
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Score 145.5; DB Pred. No. 0.024; 3; Mismatches
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Pred. No. 0.0082;
3; Mismatches 75
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82;
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A; Note: in G
C; Comment: 1
C; Genetics:
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C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyre
F;1-6/Product: gag protein (fragment) #status predicted <GAG>
F;7-59/Product: env protein (fragment) #status predicted <ENV>
F;60-698/Product: protein-tyrosine kinase erbB #status predicted <ERB>
F;194-459/Domain: protein kinase homology <KIN>
F;202-210/Region: protein kinase ATP-binding motif
F;229/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-698 <NIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: c-erbB activation in ALV-induced erythroblastosis: A;Reference number: A00643; MUID:85228222; PMID:2988784 A;Accession: B00643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, Cell 41, 719-726, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999
C;Accession: B00643; A00643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine kinase (EC 2.7.1.112) erbB - avia
N;Contains: amino end of gag protein; env protein
C;Species: avian leukosis virus, ALV
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Best Local 9
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                                                                                                                                                                                                                       DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDV 147
QINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP
                                                                                    SLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLAKTVFESSPYWIQSGNH 649
                                                                                                                                                                              DGFL-----PAPEYVNQ--LMPKKPS
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                                           -- RGAPPSTFKGTPTAENPEYLGLDVP
                                                                                                              --AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQ---- 188
                                                                                                                                                                                                                                                                                                                                                                               24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                      11.7%;
                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                        Score 138; DB
Pred. No. 0.07
25; Mismatches
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tein fragment; protei
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and

epidermal growth factor receptor precursor - chicke N;Contains: protein-tyrosine kinase (EC 2.7.1.112) C;Species: Gallus gallus (chicken) C;Date: 28-Feb-1986 #sequence_revision 05-May-1995

05-May-1995 #text_change

04 - Feb - 2000

chicken

erbB

TVCHLV

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salivary proline-rich phosphoprotein precursor PRB1 (large allele) [validated] N;Contains: peptide IB-1; peptide P-E (peptide IB-9); peptide P-F; peptide P-H C;Species: Homo sapiens (man) C;Date: 04-Dec-1986 #sequence_revision 12-Apr-1996 #text_change 08-Dec-2000 C;Accession: B40750; C40750; A40750; C25372; S02128; S02127; A03293; A90502; ASR;Azen, E.A.; Latreille, P.; Niece, R.L. R;Azen, Genet. 53, 264-278, 1993 A;Title: PRBI gene variants coding for length and null polymorphisms among huma A;Reference number: A40750; MUID:93304421; PMID:8317492
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A;Title: Chicken epidermal growth factor (EGF) receptor:
A:Boference number: A27720; MUID:88261272; PMID:3260329
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F;727-735/Region: protein kinase ATP-binding motif
F;126,202,280,361,370,422,575,580,615,335/Binding site: carbohydrate (Thr)
F;136,202,280,361,370,422,575,580,615,335/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;687/Binding site: carbohydrate (Thr) (covalent) (by protein kinase C) #status
F;754/Active site: Lys #status predicted
F;754/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;31-1223/Product: epidermal growth factor receptor #status predicted F;31-654/Domain: extracellular #status predicted <EXT> F;31-654/Domain: extracellular #status predicted <EXT> EF;31-307/Domain: EGF receptor extracellular domain repeat <EE1> F;397-610/Domain: EGF receptor extracellular domain repeat <EE2> F;655-677/Domain: transmembrane #status predicted <TMM> F;678-1223/Domain: intracellular #status predicted <INT>
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A; Residues: 585-1223
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A; Residues: 1-1223 <LAX>
A; Cross-references: GB:M20386
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                                            A; Molecule type:
                                                                   A; Accession: B40750
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Best Local S
Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ---DPPE--
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                       35-392 <AZE>
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24.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
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A; Accession: C407:
A; Molecule type:
A;Molecule type: protein
A;Residues: 92-127, 'R', 129-148, 'R', 150-152 <KA3>
R;Issmura, S; Saitoh, E; Sanada, K.
J. Biochem. 91, 2067-2075, 1982
                                                                                                             A;Reference number:
A;Contents: IB-9
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                                                                                      A; Accession: A90464
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A; Molecule type: DNA

A; Residues: 35-39, 'p',41-84,'G',86,'R',87-154,'R',218-246;300-306,'T',308-329,'C',

A; Recession: A05262

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 'N',57-59,'A',61-69;334-336,'S',338-339,'R',341-392 <AZ5>

R; Kauffman, D.; Wong, R; Bennick, A.; Keller, P.

Blochemistry 21, 6558-6562, 1982

A; Title: Basic proline-rich proteins from human parotid saliva: complete covalent
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A;Cross-references: GB:K03304; NID:
A;Ote: alternatively splice forms
R;Lyons, K.M.; Stein, J.H.; Smithle
Genetics 120, 267-278, 1988
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A; Residues: 35-183, 245-392 <LY2>
A; Cross references: EMBL: X07516
A; Cross references: EMBL: X07516
A; Cross references: EMBL: X07516
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A; Cross referenc
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A;Molecule type: DNA
A;Residues: 35-127,250-273,'R',275-277,'R',279-336,'S',338-392
A;Cross-references: EMBL:X07517
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Proc. Natl. Acad. Sci. U.S.A. 81, 5561-5565, 1984
A;Reference number: A94005; MUID:84298176; PMID:6089212
A;Accession: A05261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biochem. 94, 1991-1999, 1983
A;Title: Further fractionation of basic proline-rich peptides
A;Reference number: A91974; MUID:84161824; PMID:6671974
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A;Residues: 275-336,'S',338-392 <KAU>
R;Saitoh, E.; Isemura, S.; Sanada, K.
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A; Residues: 17-38, 'AP', 41-51, 92-148, 'R', 150-152
A; Note: among nine basic proline-rich peptides:
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A; Status: translation not shown
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A; Residues: 35-183, 245-270, 'Q', 272-392
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A;Cross-references: GB:S62929
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    A90464;
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92, 1986
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proteins from human parotid MUID:83101329; PMID:6924859
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Snature 393, 537-544, 1998

A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Bar A:Authors: Leciphering the biology of Mycobacterium tuberculosis from A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: H70786

A:Accession: H70786

A:Status: nucleic acid sequence not shown; translation not shown A:Molecule type: DNA

A:Residues: 1-53 <COL>
A:Cross-references: GB:Z70283; GB:ALL23456; NID:g3261561; PIDN:CAA94

A:Experimental source: strain H37Rv

C:Genetics:
A:Gene: sucB
C:Superfamily: Mycobacterium probable dihydrolipoamide succinyltrans F:4-77/Domain: lipoyl/biotin-binding homology <LPBI>
F:43/Binding site: lipoamide (Lys) (covalent) #status predicted
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A;Gene: GDB:PRB1
A;Cross-references: GDB:11951; OMIM:180989
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A:Contents: P-E
A:Accession: A91966
A:Accession: A91966
A:Molecule type: protein
A:Residues: 92-127,'R',129-140,'R',150-152 <ISE>
A:Residues: 92-127,'R',129-140,'R',150-152 <ISE>
C:Comment: This peptide contains 21-residue repeats, two of which have inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable dihydrolipoamide acetyltransferase component [similarity] - C;Species: Mycobacterium tuberculosis C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 01-Se C;Date: 20-Apr-2008 #sequence_revision 20-Apr-2000 #text_change 01-Se C;Accession: H70786 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Ha R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, C.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hand, C.; Connor, R.; Davies, R.; Devlin, R.; Connor, R.; Davies, R.; Devlin, R.; Feltwell, T.; Gentles, S.; Hand, C.; Connor, R.; Davies, R.; Devlin, R.; Devlin, R.; Connor, R.; Davies, R.; 
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lipoyl/biotin-binding homology <LPB1>
ite: lipoamide (Lys) (covalent) #status predicted
site: lipoamide (Lys) (covalent) #status predicted
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Score 135.5; DB
Pred. No. 0.083;
4; Mismatches
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Feltwell, T.; Gentles, S.; Hamlin, N.;
S.; Seeger, K.; Skelton, S.; Squares,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X13885; NID:g19866; PIDN:CAA32090.1; C;Superfamily: hydroxyproline-rich glycoprotein C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: I
A; Residues: 1-620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHGHPPPPTYAQPPPTPTYSPSPQVQPPPTYSPPPPTHVQPTPSPPSRGHQPQPPTHRHA 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPGHL----PSHGQRPPSPSHGHAPPSG---
                                                                                                                                                                                                                                                                                                                                                   PTYSPPPPSPIYSPPPPAYSPSPPPTPTPTF-----SPPPPAYSPPPTYSPPP----P
                                                                                                                                                                                                                                                                                                                                                                                   GGAAPQP-----HPPPAFSPA---
                                                                                                                                                                                                                                                                                                                                                                                                                        P-PTHRHAPPTHQPSPLRHLPPSPRRQPQPPTYSPPPPAYAQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLPAARPAGATLE-----RAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R-----YSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDV-----RPQPPSPREG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGDLTLGLEPSEEEAPRSPL---APSEGAGSDVFDGDLGMGAAKGLQSLPTH-DPSPLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSLPTHDPSPLQ------RYSEDPTVPLPSETD--GYVAPLTCSPQPEYVNQPDVRPQP- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPSEEEAPRSPL--APSEGAGSDVFDGDLGMGAAKG--
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                                                                                                                                                                                                                                                                                                                                                                                     ----FDNLYYWDQDPPERGAPPSTFKGTPTAENP 209
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                                                                                                            Ueno, X.Y.Z
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                                                                 C; Date: 23-Apr-1999
                                                                                 probable serine/threonine-specific protein kinase (EC
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E;ACCESSACE. D.; Stellyes, L.
R;JObnson, D.; Stellyes, L.
submitted to the EMBL Data Library, Novemb
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                                R; Bevan, M.; Terryn,
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C;Genetics:
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A; Reference number: Z20601
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               H.W.; Mayer,
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                                                                                                                                                                                   SVEPSED----
                                                                                                                                                                                                                  AFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
                                                                                                                                                                                                                                                                                LPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQP-----HPPP
                                                                                                                                                                                                                                                                                                                ----PVIASSADPILPTSVVPQPSNEPSPGTVAP---SDEPSPSGPPS---PGPVNPSEDP
                                                                                                                                                                                                                                                                                                                                                                               HHHHKTKAPRTSRGIATTTFAPTSSDL---PIAGSSSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                HHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APQPHPPPAFSPAFDNLYYWDQDPPERGAPP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSP---
                                                                                                                                                                                                                                                   QPSGPPSPGPVDPSEDPQP-
                                                                                                                                                                                                                                                                                                                                                HDPSPLQRYSEDP-----TVPLPSE--TDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RQPPTSLNGPPSPINEPAPELPQRHNSLHRKTAGPVR----GLAPPPPQSVHLSP-GGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GAPPAPSQNAKPYNR--EKPLPPTPGHRAPAAPPVKPPPSPINSRSPSAHSQPPPPPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 24.2
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---REGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPE--YLTPQGGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                 K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: U41557; PIDN: AAA83301.1; CESP: C50F7
                                                                 #sequence_revision
                                N.; Ardiles, W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.4%;
28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%;
                                                                                                                                                                                 PQPSGPPSPGPVDP-SEDPQPSGSSSP 195
                 Schueller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 134; DB 2
Pred. No. 0.055;
Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134.5; DB Pred. No. 0.064;
Database,
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                               Buysshaert, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB/EMBL/DDBJ
                                                              23-Apr-1999
                                                                                                                                                                                                                                                   ----SVEPSEDHQPSGPPSPGPVDPSEDPQP
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September 1998
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                                                               #text_change 17-Mar-2000
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                                Dasseville,
                                                                                                2.7.1.-)
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                                R.; De Clerck,
                                                                                                                                                                                                                                                                                                                 116
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                                                                                               Arabidopsis
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A; Molecule type: mRNA
A; Residues: 969-971, 'K', 973-1115, 'D'
A; Cross-references: EMBL: Z12608
R; Helsermann, G.J.; G111, G.N.
J. B101. Chem. 263, 13152-13158, 1981
A; Title: Epidermal growth factor real
                                                                                                                                                                           submitted to the EMBL Data Library, A;Reference number: S24942 A;Accession: S24942
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U03425
R;Avivi, A.; Lax, I.; Ullrich,
Oncogene 6, 673-676, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermal growth factor receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643
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                                     A; Reference number: A28941;
                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-714 <AVI>
                                                                                                                                                                                                                                                                                                                   A;Title: Comparison of EGF receptor sequences as a guide A;Reference number: A43818; MUID:91232866; PMID:2030916 A;Accession: A43818
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A; Note: T4L20.20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: AL023094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues:
                                                                                                                                                                                                                                        R;Eisinger, D.P.;
                                                                                                                                                                                                                                                             A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1210 <LUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A53183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: The mouse waved-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Luetteke, N.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; Keywords: phosphotransferase; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: A53183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG-----PLPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .C.; Phillips, H.K.; Qiu, 399-413, 1994
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                      Serrero,
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                                                                                                                                                                                                                                                             GB:X59698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phenotype results from a point mutation; MUID:94170986; PMID:8125255
                                       MUID:88330814; PMID:3138233
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                                                                             1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 134; DB Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                 Schlessinger,
                                                                                                                                                                                                                     June 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.H.; Copeland, N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QTPENPSPPAP-EGSTPVTPPAPP
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                                                                                                                                                                                                                                                                                                                                                                                                   J.; Givol,
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                                                        phosphorylate
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R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
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N.Title: Expression of the epidermal growth factor receptor gene is regulated in mouse
N.Reference number: 149643; MUID:93126380; PMID:7678348
N.Accession: I49643
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Molecule type: DNA

Residues: 1-971,'K',973-1210 <VER>
Cross-references: EMBL:X78987; NID:q488830; PIDN:CAA55587.1; PID:q488831;
Cross-references: EMBL:X78987; NID:q488830; PIDN:CAA55587.1; PID:q488831;
Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.

Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.

Paria, B.C.; Das, S.K.; Pid:q488830; PIDN:CAA55587.1; PID:q488831;
Cross-references: EMBL:X78987; NID:q488830; PIDN:CAA55587.1; PID:q488831;
Cross-references: EMBL:X78987; PID:q488830; PID:q488830; PID:q488830; PID:q488830; PID:q488830; PID:q488830; PID:q488831;
Cross-references: EMBL:X78987; PID:q488830; PID:q488830; PID:q488831; PID:q4888831; PID:q4888831; PID:q4888831; PID:q4888831; PID:q4888831; PID:q4888831; PID:q
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Residues: 12-20,22-132.<RES>
Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                         1165 MSLDNPDYQQDFFPKETKPNGIFKG-PTAENAEYLRVAPP 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 DVFDGDLGMGAAKGLQSLPTHDPSP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLSPGKNGVVKDVFAFGGAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDPTGAVTEDNIDDAFL-----PVPEYVNQ-SVPKRPAGSVQNPVYHNQPLHP----- 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDPTVPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVVDADEYLIPQQGFFNSPSTSRTPLLSSLSATSNNSTVACINRNGSCRVKEDAFLQRYS 1070
                                                                                                                                                                                                                                                                                                                                                                                                                       --APGRDLHYON--PHSNAVGNPEYLNTAQ------PTCLSSGFNSPALWIOKGSHQ 1164
                                                                                                                                                                                                                                                                                                                   ----DP-----PERGAPPSTFKGTPTAENPEYLGLDVP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ne EMBL Data Library, April 1994
The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.3%; Score 134; DB 2; 26.4%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Result
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to a score greater than or equal to the score of the result being and is derived by analysis of the total score distribution
                                                                                                                                                                                                                   Score
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa1992.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa1993.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa1993.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa1994.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa1995.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa1996.DAT:*
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/SIDS2,
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AAE13122
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AAU98923
AAY92620
AAE12130
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1660.081 Million cell updates/sec
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NY-ESO-IC-HER-2 me
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Human HER500-hGM-C
Human HER500-IGM-C
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Amino acid sequenc	2 AAB68420		13.9	164	٠.
_	AAY5061	1210 2	•	164	_
Amino acid sequenc			•	164	
Human cancer assoc			54.9	648.5	٠٠
-	AAB5887		•	711	_
Human HER-2/neu pr		1200 21	73.1	864	_
Her-2			80.7	954	_
Rat HER-2/neu prot			80.7	954	~
ည်		1256 2	81.3	961	•
seque			81.3	961	•
Mouse Her-2/neu pr			81.3	961	•
Mouse Her-2/neu ex	3 AAM51153		•	961	-
Mouse Her-2/neu ex			•	961	_
HER-2/neu polypept			•	1086	
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Human Her-2/neu po			•	1177	_
2/neu			•	1177	_
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Human Her-2 protei			•	1177	-
nino a			•	1177	•
Human HER-2/neu pr			٠	1177	•
acid seque			•	1177	
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protein	AAE2048		•	1177	-
Human protein for			•	1177	
protein				1177	•
Her-2/neu			•	1177	
`	1 AAB21201		•	7	_
n HER2 (ErbB2			•		
HER2 transgene pla	2 AAB60167		100.0	1182	

ALIGNMENTS

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RESULT 1
AAE13121
ID AAE1
XX AAE1
XX AAE1
AC AAE:
XX MAT
DT 28-
DT 28-
DT 48-
DT 48-
DT 48-
DT 48-
DT 48-
DT 78-
DT 88-
DT 78-
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N-PSDB; AAD21572.
                                                                                                                                                                                                                                                      Laus R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2000; 2000US-193504P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US10515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory fusion protein; IFP; antigen component; therapy: immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; human; HER-2 membrane distal intracellular domain.
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                                                                                                                                                                                                                                                 Vidovic D,
                                                                                                                                                                                                                                                           Graddis
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An immunostimulatory fusion protein comprising the intracellular domain

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RESULT 2
AAE13122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is mature human HER-2 membrane distal intracellular domain.
                                                                                                                                                                                                                                                           immunostimulatory
dendritic cell; cc
human; HER-2 membr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to immunostimulatory fusion nucleic acid molecules encoding such proteins. The
            N-PSDB;
                                                                                                                                 30-MAR-2001; 2001WO-US10515
                                                                                                                                                               11-OCT-2001
                                                                                                                                                                                          WO200174855-A2
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                              autoimmunogenic
                                                                                                                                                                                                                                                                                                                           NY-ESO-IC-HER-2 membrane distal intracellular domain
                                                                                                                                                                                                                                                                                                                                                         28-JAN-2002
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                                                                                                                                                                                                                                                                                                    Immunostimulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HER-2 and an antigen elicits an immune response to the antigen useful for the treatment of associated cancer associated -
                                             ,≅
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL
                         2001-662965/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is used in the HER500 and HER300 GM-CSF fusion constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL
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                                                                               DENDREON CORP
              AAD21573
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                                                   Vidovic D,
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                         2000US-193504P
                                                                                                                                                                                                                                                             membrane
                                                                                                                                                                                                                                                                     ry fusion protein; IFP; antigen component; thera ry component; T-cell mediated immune response; D colon cancer; breast carcinoma; ovarian cancer;
                                                                                                                                                                                                                                                                                                fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1182; 100.0%; Pred. No. 1
                                                   Graddis
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comports a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC) induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is a fusion protein which comprises human autoimmunogenic cancer/testis antigen, NY-ESO-IC and mature human HER-2 membrane distal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
is
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 54-55; 59pp; English
 361
                                                                                                                                                                                                                                                                                                                                                                                                     intracellular domain.
                                  181
                                                                       301
                                                                                                         121
                                                                                                                                                241
                                                                                                                                                                                                                     181 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
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                                                                                                                                                                                                                                      1 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunostimulatory fusion protein comprising the intracellular domain HER-2 and an antigen elicits an immune response to the antigen and useful for the treatment of associated cancer associated - \,
DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 397
                     DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
                                                                                                         PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPIIPPPAFSPAF
                                                                                                                                                                                  LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120
                                                                       PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF
                                                                                                                                              al Similarity
217; Conserv
                                                                                                                                                                                                                                                                                                                                                                   397 AA;
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                              Mismatches
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RESULT 3
AAE13108
Chimeric - Chimeric -
                                                                                                                                                                    dendritic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human;
                                                                                                                                                                                                                                                                                             AAE13108
                                                                                                            WO200174855-A2
                                                                                                                                                              HER-2
                                                                                                                                                                                                                                   Human HER500 fusion protein construct.
                                                                                                                                                                                                                                                       28-JAN-2002
                                                                                                                                                                                                    Immunostimulatory fusion protein; IFP; antigen component; therapy;
immunostimulatory component; T-cell mediated immune response; DC;
                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                             standard;
                                                                                                                               Synthetic
                                                                                                                                        Homo sapiens.
                                                                                                                                                              HER500 fusion
                                                                                                                                                                                                                                                                                             Protein;
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30-MAR-2000;

2000US-193504P

(DEND-) DENDREON CORP

Vidovic D,

Graddis T;

30-MAR-2001; 2001WO-US10515

11-OCT-2001

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RESULT 4
AAE13110
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X PRX FRX PRX X PR
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains and a C-terminal tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 200
N-PSDB;
                                                                                                                                                                                                                                           Chimeric -
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                                                                                                                                                                                      WO200174855-A2
                                                                                                                                                                                                                                                                                                                                                      PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; OVA;
                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory fusion protein; IFP; antigen component; therapy; immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE13110 standard; Protein; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                          30-MAR-2000; 2000US-193504P
                                                                           30-MAR-2001; 2001WO-US10515
                                                                                                                                     11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulatory fusion
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217; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and an antigen
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                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        construct comprising OVA-derived octapeptide
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Pred. No. 5.
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5.3e-91;
es 0;
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RESULT 5
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DT 28;-J
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                                                                                                                                                                                                                            PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                     Human HER500-hGM-CSF fusion protein construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE13109 standard;
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                                                                                                                                                                         HER-2 protein; granulocyte-macrophage colony stimulating
HER500-hGM-CSF fusion protein.
                                                                                                                                                                                                                                                                                     dendritic cell; colon cancer; breast carcinoma; ovarian
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immunostimulatory component; T-cell mediated immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
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Pred. No. 5.4e-91;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to immunoscimulatory comprise a nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antigen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is HER500 hGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular and intracellular domains, an Ala Ala linker, a mature human granulocyte-
                       immunostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; PAP protein; Ala Arg linker; membrane distal extracellular domain; membrane distal intracellular domain; C-terminal tag; human; GM-CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An immunostimulatory fusion protein comprising the intracellular of HER-2 and an antigen elicits an immune response to the antiger is useful for the treatment of associated cancer associated -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                          Immunostimulatory fusion protein; IFP; antigen component;
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protein;
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RESULT 7
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standard;

Protein; 1179

28-JAN-2002 AAE13123; AAE13123

(first entry)

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339 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG 61 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL

PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF

180 458

LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL

PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF

1 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMCAAKG 60

Matches Query Match Best Local

217;

Conservative

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Mismatches

Indels Length

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Similarity

100 000

Score 1182; Pred. No. 6

DB 22; 5.9e-91;

697; 0

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519 181 459 121 399

DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP

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                                                                                                                                                                                                           The invention relates to immunostimulatory fusion proteins (IFP) and nucleic acid molecules encoding such proteins. The IFPs comprise a polypeptide antiqen component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antiqen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antiqen. The present sequence is HER500 rGM-CSF fusion protein construct which comprises human PAP signal sequence, mature PAP protein, an Ala Arg linker, human HER-2 signal sequence, mature HER-2 membrane distal extracellular domain.
                                                                                                                       signal sequence, mature HER-2 membrane distal extracetulata commann, an Ala linker, an ovalbumin (OVA)-derived imunodominant octapeptide, HER-2 membrane distal intracellular domain, an Ala Ala linker, a mature distal intracellular domain, an Ala Ala linker, a mature of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation of the commandation
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                                                                 granulocyte-macrophage
a C-terminal tag.
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           AAU98923;
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                                     AAU98923 standard;
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human; HER-2 membrane distal intracellular domain; SART3-IC;
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Local Similarity '100.0%; Pred. No. 1.2e-90;
nes 217; Conservative 0; Mismatches 0;
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DB; AAD21574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion protein
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                                                                                                                                                                                                                                                                                              Gaps
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Matches 217;

Similarity

Conservative

0;

Mismatches

Indels

0

Gaps

0

60

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1006

GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGNGAAKG 1065

GAGGMYHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG

LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120

LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL

1125

PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAQQPHPPPAFSPAF 180 PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF

1126

181

DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP

121

1066

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Query Match
Best Local (
                                                                                   response against a cell comprising a target antigen (I) in a subject, treating a subject having undesired cells, for example tumour cells or virally infected cells (C), reducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynucleotide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pancreatic cancer, as well as lymphomas and leukaemias. The method is also useful in treating chronic viral infections such as those caused by hepadnaviruses, lentiviruses and the flaviviruses and pestiviruses. The present sequence represents the human breast cancer antigen, Her2 variant, used as a target
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                      Inducing a cell-mediated immune response against a target ar reducing undesired cells and stimulating presentation of an a cell, comprises administering a polynucleotide encoding a
                                                                                                                                                                                                                                                                                                               Claim 21; Page 134-138; 146pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001;
                                            Sequence
                                                                          antigen in
                                                                                                                                                                                                                                                                                  The invention relates to a method of inducing a cell-mediated immune
                                                                                                                                                                                                                                                                                                                                            an antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mincheff MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMBI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Her2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZOUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LOUK/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pell-mediated immune response; tumour; breast cancer;
rirus infection; prostate cancer; colorectal cancer;
ymphoma; leukaemia; hepadnavirus; lentivirus; herpes
                                                                                                                                                                                                                                                                                                                                                                                                                     2002-527524/56
DB; ABK86207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunodeficiency virus; HIV; flavivirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMERICAN FOUND BIOLOGICAL RES MINCHEFF M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZOUBAK S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOUKINOV D I.
                                            1223
                                                                          the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US45626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; antiviral; immunostimulant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0704232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer antigen,
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100.0%;
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 Score 1182; DB 23
Pred. No. 1.3e-90;
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                                                                                                                                                                                                                                                                                                                 English.
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                 DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ancer; pancreatic herpesvirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pestivirus
               Length
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variant
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1186 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1222

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RESULT
AAY9262
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Region
                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human heregulin 2 (Her2).
                          Region
                                                                                                                                                                        Doma in
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                                             Domair
                                                                                                     Region
                                                                                                                         Domair
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                                                                          /note-
                                                                                                      /label
                                                                                                                         /note= "suitable 624..654
/label= insertior
/note= "suitable
695..709
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/note= "suitable for for
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/note- "suitable for for
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                                                               label.
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/note= "suitable for foreign epitope insertion"
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/note= "suitable for foreign epitope' insertion"
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/note= "suitable for foreign epitope insertion"
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/note= "suitable for for
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suitable for foreign
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"suitable for foreign epitope insertion"
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"suitable for for
                 insertion_region
                                   Tyrosine_kinase_doma
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suitable for foreign epitope insertion
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                                                                                                              Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                              Cysteine_rich_domain
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       for foreign epitope insertion"
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                                                                                  insertion'
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181 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217

DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1254

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Best Local
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Gautam A,
                                                                                                                                                                                                                                                                              cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
 1158
                                                               1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     helper epitopes were identified (see features table). The method is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with
                                                                                                                           1038 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response. Subdominant CTL epitopes, antibody binding regions a cysteine residues involved in disulfide bonds are preserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Her2 can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 62; Page 193-198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA09455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-349917/30.
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20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-1999;
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                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mmunogenized forms.
                                                                             61 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL
                                                                                                                                           1 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
                 PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF 180
                                                                                                                                                                                        217;
 PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF
                                                               LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL
                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birk P,
                                                                                                                                                                                                                                                      1255
                                                                                                                                                                                        Conservative
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Birk P, Karlsson
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98US-0105011
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                                                                                                                                                                                                                                                    AA;
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/note= "suitable for for
710..730
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/note= "suitable for for
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                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nielsen
                                                                                                                                                                                        0;
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                                                                                                                                                                                       Score 1182; DB 21;
Pred. No. 1.3e-90;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as an autovaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor associated prostate cancer
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11.75
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RESULT 10
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Best Local
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                                                                                                                                                                                                            for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of gene transcripts that are expressed in antigen presenting calls (APCs), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
                                                         1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Therapeutic compound; ma
antigenic peptide; MHC;
adoptive immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE12130 standard; Protein;
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                             to their natural counterparts. Compounds of the invention are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicolette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tyrosine kinase-type receptor, HER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE12130;
                                                                                                                                                                                                                                                                                                                                                                        The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENZ ) GENZYME CORP.
                            61
                                                                        GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
             LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120
                                                       GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG 1097
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)B; AAD19731.
                                                                                                                  217;
LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Page
                                                                                                                                                                        1255 AA;
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0527487
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                                                                                                                                                                                                                                                                                                                                                                                                                                     63-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoregulatory; immune response; F
anti-cancer; breast cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; tyrosine kinase-type
                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                               Score 1182;
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                                                                                                                             DB 22;
1.3e-90;
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RESULT 11
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                                 Query Match
Best Local S
Matches 217
                                                                                                   The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. I particular, the antibody is directed against ErbB2 (also known as HER2 and plB5neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland; lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1218
                                                                                                                                                                                                                Treating tumors, particularly breast cancers, receptor and does not respond to an anti-ErbB conjugating the antibody to a maytansinoid -
                                                                                                                                                                                                                                                                N-PSDB;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; HER2;
                                                                                 Sequence
                                                                                                                                                                                           Example 3;
                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999; 99US-0141316.
16-MAR-2000; 2000US-0189844.
                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2000; 2000WO-US17229
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1 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMCAAKG 60
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                                 al Similarity
217; Conserv
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                                                                                 1255
                                                                                                                                                                                        Fig 4;
                                 Conservative
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                                                                                                                                                                                                                             which overexpress an antibody, comprises
                                Indels '
                                                       Length 1255;
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                                                                                                                   Query Match
Best Local
                                                                                         Matches
                                                                                                                                                                                                                                                                                anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovar, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ovary; stomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; panereas; prostate; bladder; ErbB2; neuronal disorder; gland disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; angiogenic disorder; immunological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
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05-OCT-2000;
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                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCHW/) SCHWALL R. (SLIW/) SLIWKOWSKI M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002.
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GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
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DB; ABK14058.
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                                                                                                                                                                                                    ξ,
                                                                                                                                                                                                                                                              invention.
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Query Match Best Local Matches

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Conservative

99.5%;

Score 1177; DB Pred. No. 6e-91; 0; Mismatches

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RESULT 13
AAB21201
                                                             The present sequence is the phosphorylation domain of the HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell-growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-)
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Sequence
                                                                                                                                                                                                                                                                                                                        Claim 2;
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                                                                                                                                                                                                                                                                                                                        Fig 10; 128pp;
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                                                                                                                                                                                                                                                                                                                                                                                        n proteins and
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ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its Deltapb fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated
                                                                                                                                                                             of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overspression correlates with a poor prognosis in breast and overspression correlates with a poor prognosis in breast and
                                                                                                                                                                                                                                                           The present sequence is that of the phosphorylation domain of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer accines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu (see AAM51143) is a member of the tyrosine kinase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                              Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
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                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation domain
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tyrosine kinase; receptor; c-erbB2; ç
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                                                                                                                                                                                                                                                                                                                                                                                2; Fig
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SMITHKLINE BEECHAM BIOLOGICALS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, especially breast, ovarian, colon, lung or prostate cancer at the transfer of the street of the street and the street of the sample order to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                      AAE20483 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific T-cells are useful for inhibiting the development
                                             Novel isolated Her-2/Neu prevention and diagnosis
                                                                                                       Hand-zimmermann S, (
Mcneill PD, Vedvick
                                                                                                                                                                 14-AUG-2000;
28-SEP-2000;
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                                                                                                                                                                                                                                     WO200214503-A2
                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                  human leukocyte antigen; HLA; vaccine; malignancy; cytostatic
                                                                                                                                                                                                                                                                                                                                               Human protein
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DB; AAD32746.
                                                                                                                                                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                          Her-2/Neu protein; immune response;
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2000US-236428P.
2001US-270520P.
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                                                                                                                                                                                                                                                                Location/Qualifiers 581..583
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k TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.6%;
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                                             of cancer, preferably by
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The invention relates to effective for eliciting a

o an isolated Her-2/Neu polypeptide composition an immune response. The invention is useful for

Example 5; Page 121-122;

129pp; English

CC eliciting an immune response in a patient, where the patient is human CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer. CC The composition is useful for the therapy and diagnosis of cancer. CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine CC and other compositions for the diagnosis, prevention and treatment of Chuman malignancies, for stimulating and/or expanding? Teclls specific for CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a CC patient. The invention is useful for stimulating a Tecll response in a CC patient. The invention is useful for stimulating a Tecll response in a CC patient, as probe or primer for nucleic acid hybridisation, to CC cell treatment of cancer in a CC polypeptide from a puriable fragments of interest, to isolate a full CC length gene from a suitable library, and to direct expression of a CC polypeptide in appropriate host cells. The composition is useful in CC prophylactic or therapeutic applications and for the treatment of cancer, CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-cc associated malignancies. The invention is useful in gene therapy. The CC present sequence is human protein for the clone HICD_native_coding_ region.

Sequence 583 AA;

Š Query Match
Best Local Similarity
Matches 216; Conserv Conservative 99.5%; 0; Score 1177; DB 23; Length 583; Pred. No. 1.5e-90; Mismatches Indels 0 Gaps 0;

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61

Ş В 424 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 483 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120

õ 밁 484 121 PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF 180 PAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF 543

Ş 밁 544 181 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 580

Search completed: April 28, 2003, 13:39:47 Job time: 18.4181 secs

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Minimum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 118 2 118 3 118 4 1118 6 118 7 118	1182 1182 1182 1182 1182 1182 1182	1000.00	217 397 554 690 697	1001010	US-09-821-883-25 US-09-821-883-27 US-09-821-883-1 US-09-821-883-3 US-09-821-883-2 US-09-821-883-4 US-09-821-883-29	Sequence 25, Appl Sequence 27, Appl Sequence 1, Appli Sequence 3, Appli Sequence 2, Appli Sequence 4, Appli Sequence 29, Appl
2 . 11 3 . 11 5 . 11 7 . 11 11 11	888888	1000.0	397 555 564 690 1179	10010	US-09-821-883-27 US-09-821-883-1 US-09-821-883-3 US-09-821-883-2 US-09-821-883-4 US-09-821-883-29	29
3 11 4 11 5 11 7 11	8 8 8 8 8	100.0	564 690 697 1179	101010	US-09-821-883-1 US-09-821-883-3 US-09-821-883-2 US-09-821-883-4 US-09-821-883-29	1,004
4 11 6 11 7 11	8888	100.0	564 690 697 1179	10	US-09-821-883-3 US-09-821-883-2 US-09-821-883-4 US-09-821-883-29	2423
5 11 7 11	888	100.0	690 697 1179	10	US-09-821-883-2 US-09-821-883-4 US-09-821-883-29	29
6 11 7 11	828	100.0	697 1179	10	US-09-821-883-4 US-09-821-883-29	4, 29
7 11	82	100.0	1179	10	US-09-821-883-29	29
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8 11	78	100.0	T255	φ.	US-09-769-508-2	Sequence 2, Appli
9 11	82	100.0	1255	10	US-09-811-123-9	Sequence 9, Appli
	82	100.0	1255	10	US-09-811-115-3	Sequence 3, Appli
	77	99.6	266	9	US-09-854-356-4	Sequence 4, Appli
	77	99.6	583	ø	us-09-930-125-9	Sequence 9, Appli
	77	99.6	587	9	US-09-930-125-8	Sequence 8, Appli
14 11	77		589	9	US-09-930-125-10	Sequence 10, Appl
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18 11	77	99.6	1255	ø	US-09-930-125-2	Sequence 2, Appli
19 11	177	99.6	1255	9	US-09-441-411-6	Sequence 6, Appli

4 4 5	43	42	41	40	39	38	37	36	35	34	ω S	32	<u>3</u> 1	30	29	28	27	26	25	24	23	22	21	20
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US-10-077-130-2 US-10-077-130-5	US-09-858-664A-2	US-09-770-689A-2	US-09-770-689A-4	US-10-060-036-159	US-09-771-161A-254	US-09-771-161A-164	US-10-086-464-17	US-09-823-240-9	US-09-814-777A-36	US-10-086-464-8	US-10-121-988-143	US-09-906-514-4	US-10-078-547-2	US-10-020-215-2	US-10-078-547-24	US-10-086-464-14	US-09-158-722-4	US:09-940-101-2	US-09-725-433-2	US-09-925-301-1232	US-10-102-806-583	US-09-870-759-118	US-09-854-356-2	US-09-854-356-14
Sequence 2, Appli Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 159, App	Sequence 254, App	Sequence 164, App	Sequence 17, Appl	Sequence 9, Appli	Sequence 36, Appl	Sequence 8, Appli	Sequence 143, App	Sequence 4, Appl1	Sequence 2, Appl1	Sequence 2, Appli	Sequence 24, Appl	Sequence 14, Appl	•	: Sequence 2, Appli	Sequence 2, Appli	Sequence 1232, Ap	Seguence 583, App	Sequence 118, App	Sequence 2, App,li	Sequence 14, Appl

ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-821-883-25
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Best Local Similarity
Matches 217; Conserv
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APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
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CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Cell-Based Immunotherapy FILE REFERENCE: 7636-0022.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/193,504 PRIOR FILING DATE: 2000-03-30
               181 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
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DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
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Pred. No. 5.3e-70;
Mismatches 0;
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Sequence

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Best Local :
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-03-30
NUMBER OF CONTROL 2000-03-30
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
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APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
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                                     ORGANISM: Artificial Sequence FEATURE:
                                                                          TYPE: PRT
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                 OTHER INFORMATION: HER500 construct
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Pred. No. 1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 564
TYPE: PRT
ORGANISM: Artificial Sequence
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Patent No. US20020061310A1
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PRIOR FILING DATE: 2000-03-30
NUMBER OF COMMENTAL PRIOR PRIOR PRIOR PRIOR DATE: 2000-03-30
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 519
               181 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
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US-09-821-883-2
; Sequence 2, Application US/09821883
; Patent No. US20020061310A1
; GENERAL INFORMATION:

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US-09-821-883-4
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CURRENT APPLICATION UMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local :
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Best Local 9
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Graddis, Thomas
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                                                                Score 1182; DB 10 Pred. No. 1.8e-69; Mismatches 0;
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Pred. No. 1.8e-69;
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
                                                                                                                                                        GENERAL INFORMATION: APPLICANT: STUART,
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Best Local Similarity
Matches 217; Conserv
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                    APPLICANT: CHAO, LORRINE A.
APPLICANT: BLUFORD, PETER
TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
FILE REFERENCE: BEBIO-111-C1
                                                                                              APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/769,508
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OTHER INFORMATION: SART-3-IC
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ORGANISM: Artificial Sequence
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o. US20020061310A1
                                                                                          MONAHAN, JOHN J.
LANGTON, BEATRICE
HANCOCK, MIRIAM E
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SEQ ID NO 2

SOFTWARE: PatentIn

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CURRENT FILING DATE: NUMBER OF SEQ ID NOS:

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-769-508-2
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Best Local Similarity 100
Matches 217; Conservative
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Best Local Similarity 100.0%;
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Patent No. US20020001587A1
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PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
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APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-115-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09854356 Patent No. US20020177567A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 3
                                                                                                                                                                                                                                                SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity
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OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu -09-854-356-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
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APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/493,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 014058-009810PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cheever, Martin A. APPLICANT: Gheysen, Dirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER:
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                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Pred. No. 3.3e-69;
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RESULT 13
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US-09-930-125-9
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Best Local S
Matches 216
Sequence 8, Application US/09930125
Publication No. US20020193329A1
GENERAL INFORMATION:
APPLICANT: Hand-Zimmerman, Susan
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SEQ ID NO 9
LENGTH: 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McNeill, Patricia D.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS TITLE OF INVENTION: OF HER-2/MEU-ASSOCIATED MALIGNANCIES FILE REFERENCE: 210121.544
CURRENT FILING DATE: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 216; Conserv
                                                                                                                                                                                                                                                                                              1. GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG
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PAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF 228
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                                                                                                             DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 580
                                                                                                                                                                 PAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF
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Pred. No. 3.1e-69;
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Pred. No. 1.4e-69;
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/930,125;
CURRENT FILING DATE: 2001-08-14;
NUMBER OF SEQ ID NOS: 25;
SOETWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 8;
LENGTH: 587;
TYPE: PRT;
ORGANISM: Homo Sapiens
US-09-930-125-8
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                     Query Match
Best Local Similarity
Matches 216; Conser
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Matches 216; Conserv
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APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED
FILE REFERENCE: 210121.544
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TITLE OF INVENTION: COMPOSITIONS AND METHDOS
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED
FILE REFERENCE: 210121.544
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Kalos, Michael D.
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Pred. No. 3.2e-69;
0; Mismatches 1
                                                                     Score 1177; DB 9; Pred. No. 3.2e-69; 0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 600
TYPE: PRT
ORGANISM: Homo sapiens
US-09-930-125-11
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Search completed: April 28, 2003, 13:44:07 Job time: 7.98328 secs
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Best Local Similarity 99.5
Matches 216; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT:
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PPLICANT: VedVick, Thomas S.

ITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS

ITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES

ILE REFERENCE: 210121.544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Hand-Zimmerman, Susan
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                                                                                                                                                                 61 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120
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                                                                      181 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
                                                                                                               PAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF 562
                                                      DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 599
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1: /cgn2_6/ptodata/1

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US-08-416-348A-68
US-08-465-101-2
US-08-466-545B-68
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US-08-466-680B-68
US-08-484-438-7
US-08-484-438-7
US-08-484-438-6
US-08-484-438-6
US-08-484-438-6
US-08-484-438-6
US-08-484-438-2
US-08-237-401A-4
US-08-237-401A-4
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US-08-317-310A-64
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US-08-325-737-2
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US-09-570-573-18 US-09-548-608-18 US-09-588-887-9 US-09-599-181-2 US-09-579-181-2 US-09-599-181-1 US-08-668-4 US-09-129-668-4 US-09-041-886-23 US-09-041-886-23 US-09-083-521-7 US-08-459-568-2 US-08-516-8594-2 US-08-516-8594-2 US-08-217-327-4 ALIGNMENTS			-	-	-	ω	N	N	ω	ω			w							
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TOPOLOGY:
US-08-414-417B-69
Best Loc
Matches
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                                   Query Match
                                                                                                                                                            TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/414
ETILING DATE: 31-MAR-1995
CLASSIETICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DISIS, MATY L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALISNANCIES
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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6300 Columbia Center,
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Score 1177; DB 1;
Pred. No. 3.3e-96;
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Best Local Similarity
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                                                                                                                                                                                                                 Matches
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TELEFAX: (206) 682-60
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, VACURRENT APPLICATION DATA: US/08/486,348A APPLICATION NUMBER: US/08/486,348A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/New PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/New ONCOGENE IS ASSOCIATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sharkey, Richard G. REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
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No. 5846538
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 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
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                                                                                        LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL
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Disis, mary
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Pred. No. 3
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Best Local Similarity
Matches 216; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 580 amino acids
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             181 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
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DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 579
                                                                  PAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF
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Pred. No. 3.3e-96;
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US-08-466-680B-69

Sequence 69, Application US/08466680B Patent No. 6075122

GENERAL INFORMATION:

APPLICANT:

Cheever, Martin A. Disis, Mary L.

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                                                                                                                                                                                                Patent No.
                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                              APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUN
TITLE OF INVENTION: FOR D
TITLE OF INVENTION: HER-2
                                                               CORRESPONDENCE ADDRESS
                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION: 424
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                                                ADDRESSEE:
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5726023
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Washington
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                                E: Seed and Berry 6300 Columbia Center,
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SYSTEM: PC-DOS/MS-DOS
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                                                                                              IMMUNE REACTIVITY TO HER-2/NEU PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/NEU ONCOGENE IS ASSOCIATED
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Best Local Similarity
Matches 216; Conserv
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                     APPLICANT: Cheever, Marti
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUN
TITLE OF INVENTION: FOR D
TITLE OF INVENTION: HER-2
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APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
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                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1038 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG 1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sharkey, Richa
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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NO. 5801005
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                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                           Application US/08414417B
                                                                                                                                                    E: Seed and Berry LLP 6300 Columbia Center,
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                                                                                                                                                                                                                       IMMUNE REACTIVITY TO HER-2/neu PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES HER-2/neu ONCOGENE IS ASSOCIATED
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Pred. No. 8.5e-96;
0; Mismatches 1
                                                                                                                                                    701 Fifth Avenue
   Version #1.25
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US-08-486-348A-68
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Best Local Similarity
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Patent No. 5846538
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
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               REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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CORRESPONDENCE ADDRESS:
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APPLICANT: Disis, Mary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                          APPLICATION NUMBER: US/08/486,348A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                       Sharkey, Richard G.
                                                                                                                                                                                                                                                                                                                   Washington
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31-MAR-1995
682-6031
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                                                     920010.448C6
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Pred. No. 8.5e-96;
0; Mismatches 1
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Matches 216;
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Best Local 9
                              Query Match
Best Local Similarity 99. Matches 216; Conservative
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                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/625,101
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: COMPO
TITLE OF INVENTION: REACT
TITLE OF INVENTION: OR TR
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                                                                                    MOLECULE TYPE:
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                                                                                                    TOPOLOGY:
                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                           FILING DATE: 01
CLASSIFICATION:
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                                                                                                                                  LENGTH:
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              99.5%;
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              Score 1177; DB 2; Pred. No. 8.5e-96;
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                                Length 1255;
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Best Local Similarity
Matches 216; Conserv
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Patent No. 5
                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
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                                                                                                                1038
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NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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APPLICANT: Disis, Mary
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                               1 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG 60
                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                               LQSLPTHDPSPLQRYSEDPTVPLDSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120
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                                                                                                              GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG 1097
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                                              LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 1157
98104-7092
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5876712
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                                                                                                                                                                           Score 1177; DB 2;
Pred. No. 8.5e-96;
0; Mismatches 1;
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APPLICANT: Hou...

APPLICANT: Ring, Daviu ...

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APPLICANT: Ring, Daviu ...

APPLICANT: Ring, Daviu ...

TITLE OF INVENTION: Blosynthetic ...

TITLE OF INVENTION: Marker

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault

CTREET: Exchange Place, 53 State Street
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US-08-356-786-2
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                                                                                                                                                                                                                                                     Best Local Similarity Matches 216; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,
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                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                    1 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG 60
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              DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
                                                          DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 125
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US-08-484-438-8
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US-08-466-680B-68
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                                                                                         Patent No. 5811098
Patent No. 5811098 5780031
                                                                                                                              Sequence 8, Application US/08484438
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Best Local Similarity
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Patent No. 6
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                                                                          GENERAL INFORMATION:
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APPLICANT: Cheeve
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LENGTH: 1255 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/466,680B
FILING DATE: 06-UN-1995
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 APPLICANT
                                       APPLICANT:
                                                          APPLICANT:
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TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                  61 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120
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Washington
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Plowman, Gregory D.
Culouscou, Jean-Michel
Shoyab, Mohammed
Siegall, Clay B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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RESULT 13 US-08-484-438-7

Sequence 7, Applica Patent No. 5811098 Patent No. 5811098

Application US/08484438

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APPLICANT: Hellstr m,
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
1218
                                                                                                                                1098 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 1157
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LENGTH: 1255 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                   1038 GAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKG 1097
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               181 DNLYYWDQDPPERGAPPSTFKGTPT-AENPEYLGLDVP 217
                                                                                                121 PAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
                                                                                                                                                                 61 LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL 120
                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                E: New York
TRY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                     Similarity
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(212) 869-8864/9741
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Hellstr m, Karl E.
VENTION: HER4 HUMAN RECEPTOR TYROSINE
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                    unknown
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99.1%;
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of the Americas
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                                                                                                                                                                                                                                                                   Mismatches
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SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION WITHER
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1177 FPKEAKPNGIFKGS-TAENAEYL 1198
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
07/981/165
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TITLE OF INVENTION:
                                                                                                                                       1083
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FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
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TELEX: 66141
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                                                                                     VEAFGGAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-------DP------ 190
                                                                                                                                                                                                                                       SEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET- 87
                                -PERGAPPSTFKGTPTAENPEYL 212
                                                                                                                                   DDTFL-----PVPEYINQ-SVPKRPAGSVQNPVYHNQPLNP-----APSRDPHYQD 1127
                                                                                                                                                                     -DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKD 146
                                                                                                                                                                                                     SSPSTSRTPLLSSLSATSN--NSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSI 1082
                                                                --PHSTAVGNPEYLNTVQ------PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDF 1176
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1155 Avenue of the Americas
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Hellstr m, Karl E.
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Pred. No. 2.5e-06;
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US-08-484-438-6
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US-08-475-035-4
                                                                            Sequence 6, Application US, Patent No. 5811098
Patent No. 5811098 5780031
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Best Local S
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                                                                 GENERAL
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                            APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                          191 -PERGAPPSTFKGTPTAENPEYL 212
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nes 62; Conserv
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FILING DATE: 7 Jun 1995
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FPKEAKPNGIFKGS-TAENAEYL 1198
                                                                                                                                                                                                                                                           --PHSTAVGNPEYLNTVQ------PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDF 1176
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                                                                                                                                                                                                                                                                                                                                          -DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKD 146
                                                                                                                                                                                                                                                                                                                                                                                        SSPSTSRTPLLSSLSATSN--NSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSI 1082
                                                             INFORMATION:
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                                                                                                            Application US/08484438
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Plowman, Gregory D.
Culouscou, Jean-Michel
Shoyab, Mohammed
Siegall, Clay B.
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127 Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33,438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 164; DB 2;
Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1210;
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Search completed: April 28, 2003, 13:43:20 Job time: 8.35033 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 13.3%; Score 157; DB 2; Length 541; Best Local Similarity 24.2%; Pred. No. 3.9e-06; Matches 62; Conservative 23; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 541 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                        503 QNGRIRPIVAENPEYL 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
                                                                                                                                                443 NTFANTLGKAEYLKNNILSMPEKAKKAFDNPDYWNHSLPPRSTLQHPDYLQEYSTKYFYK 502
                                                                                                                                                                                                                            409 -----
                                                                                                                                                                                                                                             360 RYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVE-----ENPFVSRR-- 408
                                                                                                                                                                                                                                                                                                                                                                        300 RDGGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCNGTLRKPVAPHVQEDSSTQ 359
                                                                                                                                                                                                                                                                                                                                   74 RYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPA 126
                                                                                                                                                                                                                                                                                                                                                                                                             16 RSGGGDLTLGLE-PSEEEAPRSPLAP-SEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : New York
E: New York
TRY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hellstr m, Ingegerd
Hellstr m, Karl E.
                                                                                                           --AENPEYL 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                      -KNGDLQ-----ALDNPEYHNASNG-----PPKAEDEYVNEPLYL
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                                                                                                                                                                                   --FSPAFDNLYYWDQDPPERGA--PPSTFKGTPT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
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Title:
Perfect score:
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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                                                                                                                                                                                           1026
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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1182
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sp_rvirus:*
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      1259
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165
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O18735 canis famil
Q8872x1 mus musculu
Q14256 homo sapien
Q8wyv0 homo sapien
Q9w6f6 gallus gall
Q8x27 drosophila
Q9yzc2 drosophila
Q9yzc2 drosophila
Q9yz70 rattus norv
Q41935 murid herpe
Q08805 homo sapien
Q39495 cylindrothe
Q39495 cylindrothe
Q9ep98 mus musculu
Q16038 homo sapien
Q91810 xenopus lae
Q18751 caenorhabdi
Q00599 homo sapien
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•	126	126	126.5	126.5	127	127	127.5	127.5	127.5	127.5	128	129	129.5	129.5	130	130	130	130.5	130.5	130.5	131	131.5	132.5	132.5	132.5	132.5	133.5	133.5	134
	10.7	10.7	10.7	10.7	10.7	10.7	10.8	10.8		10.8	•	10.9	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.1	11.1	11.2	11.2	11.2	11.2	11.3	11.3	11.3
	990	562	734	356	763	369	3179	955	594	551	889	440	1620	476	3342	3325	847	2135	2135	1480	903	473	584	487	442	322	530	440	674
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	Q9UG03	Q92JX1	088970	Q9Q0B5	Q9XDH2	Q40692	Q8V2A4	Q94F92	Q9DF69	013003	Q9F2N5	QBTF74	Q8VI59	Q9XTT6	Q9E6N3	Q9IBT9	Q9XIB6	Q9UIV7	043157	296204	Q9UPX1	Q39620	Q9FCJ3	Q8VDA4	Q39494	Q09084	008934	Q8TE44	065672
	7	Q92jx1 rhizobium m		Q9q0b5 herpes simp	=				Q9df69 gallus gall			Q8tf74 homo sapien	Q8v159 mus musculu	caenorha	turkey		Q9x1b6 arabidopsis		homo	homo	Q9upx1 homo sapien	.039620 chlamydomon	. Q9fcj3 streptomyce			lyc	O08934 mus musculu	Q8te44 homo sapien	O65672 arabidopsis

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Query Match
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Best Local
                                                                                        Q14256;
Q14256;
Q1-NOV-1996;
Q1-NOV-1996;
Q1-DEC-2001;
                                                 C-erb B2/neu
C-ERB B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ EMBL; BC027080; AAH27080.1; -.
Hypothetical protein.
SEQUENCE 367 AA; 40163 MW; 0BE03395F9E101F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 40.2 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1157
    Eukaryota;
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01-JUN-2002
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                            HOMO
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ryota; Metazoa;
                                                                                                                                                                                                                                                                                                                        DNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQSLSPHDLSPLQRYSEDPTLPLPPETDGYVAPLACSPQPEYVNQPEVRPQSPLTPEGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPL
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                                                                 6 (TrEMBLrel. 01, 0
6 (TrEMBLrel. 01, 1
1 (TrEMBLrel. 19, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                   PRELIMINARY;
                       (Human)
  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.3%;
82.0%;
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                                                                   (Fragment).
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Pred. No. 1.2e-64;
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                                                                                                                                                                                 PRT;
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  Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBE03395F9E101B0 CRC64;
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  Vertebrata;
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    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
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Q8WYV0
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Best Local Similarity 100.0%;
Matches 165; Conservative
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NON_TER
SEQUENCE
                                                                                                                                                                                                 "Novel human cDNA clones with function of inhi growth.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ EMBL; AF318349; AAL55856.1; -. InterPro; IPR002048; EF hand. InterPro; IPR000719; Euk_pkinase. InterPro; IPR0001245; Tyr_pkinase. InterPro; IPR0001245; Tyr_motif.
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MEDINE-86070181; PubMed-2999974;

COUSSENS L., Yang-Feng T.L., Liao Y.C., Che
Seeburg P.H., Libermann T.A., Schlessinger
Levinson A., Ullrich A.;

"Tyrosine kinase receptor with extensive ho
shares chromosomal location with neu oncoge
Science 230:1132-1139(1985).
                                                                 ProDom; pD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKC; 1.
PROSITE: PS00018; EF_HAND; UNKNOWN_1.
PROSITE: PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TYEMBLYEL. 20, Created)
01-MAR-2002 (TYEMBLYEL. 20, Last sequence update)
01-JUN-2002 (TYEMBLYEL. 21, Last annotation updat
Hypothetical 44.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-94000386; PubMed-8104414;

Sarkar F.H., Ball D.E., L1 Y.W., Crissman J.D.;

"Molecular cloning and sequencing of an intron of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
                                                                                                                                                          Pfam; PF00069; pkinase; Pfam; PF02757; YLP; 2.
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Wan D.F., Gu J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8WYV0;
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                       Hypothetical protein SEQUENCE 412 AA;
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Cell Biol. 12:611-615(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                         44702 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                        Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                         034397FF3F27D2BC
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J., Francke
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                         CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                            ₩.×.,
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Neoqnathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                        PRINTS; PRO0109; TYRKINASE.
Probom; PD000001; Euk_pkinase;
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                             PROSITE: PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                         Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain;
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InterPro;
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InterPro;
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                                                    Kinase;
                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                 Dixon M.,
                                                                                                                                                    Pfam; PF02757;
                                                                                                                                                                                                                                                             HSSP; P11362;
                                                                                                                                                                                                                                                                                                                           MEDLINE-99263203;
                                                                                                                                                                                                                                                                                                                                      FISSUE-HINDBRAIN;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                            InterPro; IPR001245; Tyr_pkinase
InterPro; IPR004019; YLP_motif.
                                                                                                                                                                                                                             [nterPro;
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                                                                                                                                                                                                                                                                       AF121963; AAD31764.1;
                                                   Tyrosine-protein kinase
                                                              PS00652; THER_NGER_1; UNKNOWN_1
                                                                                                                                                                                                                   IPR001368; TNFR_c6.
                                                                                                                                                                                                                                      IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                 IPR000494; EGFR_L_domain
                                                                                                                                                                                                                                                                                                                 Lumsden A.;
                                                                                                                                                                                                                             IPR002174; Furin-like.
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Pred. No. 1.4e-59;
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                                4D616436F87DC84F CRC64;
165.5; DB 1
No. 0.00024;
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           13;
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                                                                            Q9VZC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY071124; AAL48746.1; -. SEQUENCE 420 AA; 42947 MW; 96D62FFDC9F996E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8SZ47
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                                                                                                                                                                                                           QPG----
                                                                                                                                                                                                                                                            FKGTPTAENPEYLGLDVP 217
                                                                                                                                                                                                                                                                                                                                                                   VKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDP----PERGAPPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGP--LPAARPAGATLERAKTLSPGKNGV
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Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn
Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fielschmann
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guna P., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Programmer M., Programm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. CG15021 protein. CG15021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR003882; Pistil_extensin.
Interpro; IPR003882; P_iich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG15021.

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0035544; CG15021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abbil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM'N.A.
         164
                                                                                                                                                                                        117
                                                                                              144
                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 PRSPLAPSEGAGSDVFDGDLGMGAAKGL-----
                                                                                    VKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDP----PERGAPPST
                                                                                                                                                                                                                                                                        ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGP--LPAARPAGATLERAKTLSPGKNGV
                                                                                                                                                                                                                                                                                                                                                                  PSVPF-PPPGSGNGIEDSGIGPGPAPSAPAPSYGPPQTRPPPPPPPPQ-----PTPPAPR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
57; Conserv
                                                                                                                                                                                   -YGPPQTQPPRPPPQPTPSA-PAPPPPSYGPPQTPPPRPPPQPTPSA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
-PAPPPSYGPPQ----TPPPRPPPQPTPSAPAPSYGPPQPPAPQPPSPPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSTLEXTENSIN. A; 45728 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 144.5; DB 5;
Pred. No. 0.0032;
1; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A2C9CE02A07F0542 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QSLPTHDPSPLQRYSEDPTVPLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zheng L.,
Smith H.O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn
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                                                                                                                                                                                                                                                                   143
                                                                                         199
                                                                                                                                                                              163
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Matches
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                                                                        1070
                                                                                                                                                                                                                                                                                                             ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

ATP-binding; Receptor; Transferase; Tyros
                                                                                                                                                  1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-FISHER; TISSUE-LIVER;
Guttridge K., Dawson T.L., E
Submitted (NOV-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-FISHER; TISSUE-LIVER;
Petch L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-FISHER; TISSUE-LIVER;
MEDLINE-90258888; PubMed-234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9QX70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M37394; AAF14008.1; HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A truncated, secreted form of the epidermal growth factor receptor encoded by an alternatively spliced transcript in normal rat tissue Mol. Cell. Biol. 10:2973-2982(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9QX70;
                                    135
                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002174;
InterPro; IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200
                                                                                                            77
                                                                                                                                                                                     47 DVFDGDLGMGAAKGLQSLPTHDPSP------
                                                                                                                                                                                                                                            Local
                                TLSPGKNGVVKDVFAFGGAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ----- 188
                                                                                               EDPTVPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAK 134
-- APGRDLHYQN--PHSNAVSNPEYLNTAQ--
                                                                                                                                                DVVDADEYLIPQQGFFNSPSTSRTPLLSSLSANSNSSTVACINRNGSCRVKEDAFLQRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKGTPTAENPEYLGLDVP
                                                                        SDPTSVLTEDNIDDTFL-----PVPEYINQ-SVPKRPAGSVQNPVYHNQPLHP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00069; pkinase; 1.
PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00757; Furin-like; 1.
                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                               1209 AA;
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                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2342466;
s J., Raymond V.W.,
                                                                                                                                                                                                                                                                                                 134891 MW;
                                                                                                                                                                                                                                          12.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyr_pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euk_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223
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                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Earp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Earp H.S.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                          Score 144;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                               se; Tyrosine-protein kinase
96FEE7F6CC1B7773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1209
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                                                                                                                                                                                                                                                           DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
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                                                                                                                                                                                                                                                           Length 1209;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                       ----LQRYS
                                                                                                                                                                                                                           76;
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RESULT 10
Q08805
ID Q0880
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DT Q1-NO
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DE PRBLL
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OC ELKAN
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RP SEQUE
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Best Local S
Matches 60
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041935;
01-JAN-1998
01-JAN-1998
01-JUN-2000
                                                                                                                              Q08805;
Q08805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1164
                                                                                                                                                                                                                                                                                                                                                                                                           Latreille P., Wamsley P., Wassubmitted (APR-1997) to the:
EMBL; U97553; AAB66392.1; -. Hypothetical protein.
SEQUENCE 585 AA; 60160 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murid herpesvirus 4.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical GAMMAHV.M6.
                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, PRBIL protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virgin H.W. IV, Latreille P.,
Dal Canto A.J., Speck S.H.;
SEQUENCE FROM N.A. MEDLINE-93304421;
                                                PRBIL.
Homo saplens (Human).
Motazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gammaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-WUMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97366649; PubMed=9223479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=33708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
                                                                                                                                                                                                                  183
                                                                                                                                                                                                                                        323
                                                                                                                                                                                                                                                            130
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                                                                                                                                                                                                                                                                                 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virol. 71:5894-5904(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAGARIP
                                                                                                                                                                                                                                        IPDL----PGP---
                                                                                                                                                                                                                                                        LERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQ-PHPPPAFSPAFDN-----
                                                                                                                                                                                                                                                                               ELGPGSP--TSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAGAR
                                                                                                                                                                                                                                                                                                     TDGYVAPLTCSPQPEYVNQ---
                                                                                                                                                                                                                                                                                                                         PSWGPDPRPPRPPPELGPGSPTSPAPSRAGA----RIPDL-PGPLPSWGPDPRPPRPPP
                                                                                                                                                                                                                                                                                                                                            PSEEEAPRSPLAPSE-GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSE
                                                                                                                                                                                                                                                                                                                                                                    60;
                                                                                                                                                                                                                                                                                                                                                                   Similarity 26.1
50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                 -----LYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
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                                                                                                                                        PRELIMINARY;
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 PubMed-8317492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and genomic analysis
                                          Primates;
                                                                                                                                                                                                                                                                                                                                                                                                            60160 MW;
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                                                                                             Created)
Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                  Score 140; DB 12
Pred. No. 0.0094;
8; Mismatches 9
                                         Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wamsley
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                                                                                                                                                                                                                                      -- LPSWGPDPRPPRPPPELGPGSPTSPAPSR
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                                          Hominidae;
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                                                    Euteleostomi;
                                          Homo
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Best Local s
Matches 59
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Q39495;
                                                                                                                                                                                                                                                    Eur. J.
                                                                                                                                                                                                                                                                                  MEDLINE-96314479; PubMed-8706728;
Kroeger N., Bergsdorf C., Sumper M.;
"Frustulins:Domain_conversation in a
                                                                                                                                                                                                                                                                                                                                             Cylindrotheca fusiformis (Marine diatom).
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Bacillariales; Bacillariaceae; Cylindrotheca.
NCBI_TaxID-2853;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **Azen E.A., Latreille P., Niece R.L.;

**PRBI gene variants coding for length and null po human salivary Ps, PmF, PmS, and Pe proline-rich hum. Genet. 53:264-278(1993).
                                                                                                                                                                                                                                                                                                                                                                                               FRU ALPHA 2
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                                                                                                                                                                                                                                                                       diatom cell walls."
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                                               215
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275
                       156
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                                                                                                                                                                                                      Joca 1
                                            GPTPASAPSGGDPPVKATYDFPLGLCEGDCDDDPDCEDGLICFQRDANESVPGCSGGSSD
                                                                                                           ---LPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQP----PSPRE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PPPQGDKSQSPRSP-PGKPQG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSRSPRSPPGK-PQGPPPQGGNQPQGPPPPPGKPQGPPPQGGNKPQGPPPPGKPQG----
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 RSRTDYCIKENPSTPPPTPPPAPAP
                      --NPEYLTPQGGAAPQPHPPPAFSP
                                                                    GPLPAARPAG----
                                                                                             APTVPTADPSP-----DPT-PDPSPDP----
                                                                                                                                           PGVPLERCEGDCDSDSECASSDLFCFPRNDDVVVPGCRGGQSDDSKFDYCIRRVDAPPGV
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x99327; CAA67702.1; -.
                                                                                                                                                                                          1 Similarity
57; Conserv
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59; Conser
                                                                                                                                                                                                                                        438 AA;
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ilarity 26.6%;
Conservative 1
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                                                                                                                                                                                                                                         45947 MW; 3F894F5033634B03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35050 MW;
                                                                     -ATLERAKTLSPG-----KNGVV---KDV----FAFGGAVE
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Last sequence up
Last annotation
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Pred. No. 0.00
17; Mismatches
                                                                                                                                                                                                     Score 136.5;
Pred. No. 0.
                      178
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                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                     No. 0.012;
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                                                                                                                                                                                                                                                                                      protein
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                                               274
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Best Local
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Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tridermal growth factor receptor isoform 1.
1071
                                                                                  1011
                                                                                                                                                                                                                                                                PROSITE; PS0019: CYTOCHROME_C: UNKNOWN_1.
PROSITE; PS00107: PROTEIN_KINASE_ATP: 1.
PROSITE; PS00109: PROTEIN_KINASE_TVR: 1.
PROSITE; PS00109: PROTEIN_KINASE_TVR: 1.
ATP-binding: Receptor: Transferase.
                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain;
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
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Schehl C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC; Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Sinclair C.S., Pearsail R.S., Green P.J., Yee D., Lam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9EP98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002290;
InterPro; IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR00034
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                                         77
                                                                                                                        47
SDPTGAVTEDNIDDAFL
                                                                             DVVDADEYLTPQQGFFNSPSTSRTPLLSSLSATSNNSTVACINRNGSCRVKEDAFLQRYS
                                                                                                                    DVFDGDLGMGAAKGLQSLPTHDPSP-----
                                      EDPTVPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P11362; 1FGK
                                                                                                                                                                                                                                                                                                                                                                      SM00261; FU; 5.
SM00220; S_TKC; 1.
SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   SM00261; FU;
                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002174;
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                                                                                                                                                                 Conservative
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AAG28045.1;
AAG28045.1;
AAG24386.1;
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Rodentia;
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; EGFR_L_domain.
; Euk_pkinase.
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Crossley T.O., Magnuson T.R.,
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PVPEYVNQ-SVPKRPAGSVQNPVYHNQPLHP---
                                                                                                                                                               Pred. No. 0.0
3; Mismatches
                                                                                                                                                                                 Score 136; DB 11;
Pred. No. 0.043;
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d A.L.,
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Matches 64
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                              Proline rich protein.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Lamphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                          01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1165
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"PRBI gene variants coding for length and null polymorphisms among human salivary Ps, PmF, PmS, and Pe proline-rich proteins (PRPs).";
Am. J. Hum. Genet. 53:264-278(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q16038
NCBI_TaxID=8355;
                     Xenopodinae;
                                                                                                             091810;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                               ----PPPQGDKSQSPRSP-PGKPQG---
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                                                                                                (TrEMBLrel.
                                                                                                                       PRELIMINARY;
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                       Xenopus
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Primates;
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Last sequential Last anno
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                                           Vertebrata; Euteleostomi;
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Best Local 9
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01-NOV-1996 (TrEMBLrel. 01, C.
01-NOV-1996 (TrEMBLrel. 01, L.
01-DEC-2001 (TrEMBLrel. 19, L.
C50F7.5 protein.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishimatsu S.I., Satoshi, Oda, Naoto, Ueno;
Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; X68249; CAA48321.1;
InterPro; IPR003124; WH2.
Pfam; PF02205; WH2; 1.
PRINTS; PR01574; TUBBYPROTEIN.
SMART; SM00246; WH2; 1.
SEQUENCE 379 AA; 38859 MW; 84DC0FB24F971AAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q18751
                                                                                                                                                                             SEQUENCE FROM N.A.
Johnson, D, Stellyes L.;
"The sequence of C. elegans submitted (DEC-1995) to the
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases EMBL; U41557; AAA83301.1; -. SEQUENCE 309 AA; 31085 MW; 6171574A991696D7 CRC64;
                                                                                           Waterston R.;
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Rhabditidae; Pelode;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGGRPHDDSDSGSNRSSPPEVGRAHRPSLPDLSRPPSSTSSGMKHSSSAPPPPPPGRRQA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RP---PPPA------RDPPGRGAAP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----REGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPE--YLTPQGGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GAPPAPSQNAKPYNR--EKPLPPTPGHRAPAAPPVKPPPSPINSRSPSAHSQPPPPPPY 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSP--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 11.4%; Score 134.5; Similarity 28.0%; Pred. No. 0.01 59; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Peloderinae; Caenorhabditis.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                cosmid C50F7.";
EMBL/GenBank/DDBJ databases
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 163
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                                                                                                                                                   67
                                                                                                                                                                                 31 HHHHKTKAPRTSRGIATTTFAPTSSDL---PIAGSSSA-----
                                                                                                                                                                                                              7 HHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPT 66
                                                                                        LPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQP-----HPPP 174
 SVEPSED
                                                                                                                                                 HDPSPLQRYSEDP-----TVPLPSE--TDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGP 119
                                                          QPSGPPSPGPVDPSEDPQP-----SVEPSEDHQPSGPPSPGPVDPSEDPQP 162
                            AFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 217
                                                                                                                       ----PVIASSADPILPTSVVPQPSNEPSPGTVAP---SDEPSPSGPPS--PGPVNPSEDP 116
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                            11.3%;
24.2%;
PQPSGPPSPGPVDP-SEDPQPSGSSSP 195
                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                            Score 134; DB 5
Pred. No. 0.013;
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                          DB 5; Length 309
                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                          Gaps
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